

DR Genew; HGNC:6722; LU.
 DR MIM: 111200; -.
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004888; F: transmembrane receptor activity; TAS.
 DR GO: GO:0007155; P: cell adhesion; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; Ig_5.
 DR SMART: SM00408; IGc2; 2.
 DR PROSITE: PS50835; IG-LIKE; 5.
 DR Receptor; Immunoglobulin domain; Glycoprotein; Transmembrane; Signal;
 KW Repeat; Blood group antigen.
 FT SIGNAL 1 31
 FT CHAIN 32 628 LUTHERAN BLOOD GROUP GLYCOPROTEIN.
 FT DOMAIN 32 547 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 548 568 POTENTIAL.
 FT DOMAIN 569 628 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 142 IG-LIKE V-TYPE 1.
 FT DOMAIN 147 252 IG-LIKE V-TYPE 2.
 FT DOMAIN 274 355 IG-LIKE C2-TYPE 1.
 FT DOMAIN 363 441 IG-LIKE C2-TYPE 2.
 FT DOMAIN 448 541 IG-LIKE C2-TYPE 3.
 FT DOMAIN 53 125 PROBABLE.
 FT DISULFID 172 237 PROBABLE.
 FT DISULFID 291 337 PROBABLE.
 FT DISULFID 384 424 PROBABLE.
 FT DISULFID 473 522 PROBABLE.
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 225 226 EL -> DV (IN REF. 2).
 FT CONFLICT 355 356
 SQ SEQUENCE 628 AA; 67374 MW; C69B0A4835492B1E CRC64;
 . Query Match 7.3%; Score 96; DB 1; Length 628;
 . Best Local Similarity 24.1%; Pred. No. 6.6;
 . Matches 66; Conservative 33; Mismatches 89; Indels 86; Gaps 16;
 QY 32 KKGPVETLTASQKSIQFMKNSNQIKLGNQGSFLTKGPKSLNBRADSRSLMDQGN 91
 Db 282 REGTVQLCGDGSPEPTL-----FRLQDEQEVLANVNEGN 321
 QY 92 PFLIIKLIKEDSDTYICEVE--DQKEVQV--LVFGLTNSDTHLLQGSLTLTLESP 146
 Db 322 --LTLEGVTRGSGTYGCRVEDYDAADVQSKTLELRVAVLDPLEISEGKVLSTL---P 375
 QY 147 RGSPPVQC-----RSPRGKNIQGGKTLVSQLELDQSGTWC-----TV 186
 Db 376 LNSSAVNCSVHGLPTPALRTKSTPLG---DGPMLSLSTIFDSNGTVVCSASLPTV 431
 QY 187 -----LQV-----QKQVEFK-IDIVPRAS-----ALPAPPTGSLPDPOTA-SALP 225
 Db 432 PVLSTQNFITLVGGSPELKTAEIEPKADGSGWRGDEVTLLCSARGH--PDPKLSWSQLG 489
 QY 226 DPPASALPALAVISFLGLL-----GVAC 252
 Db 490 GSP-AEPIPRGQGWVSSLLTKVTSAISRDISC 522
 RESULT 94
 VGR3_MOUSE STANDARD; PRT; 1363 AA.
 AC P35917;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
 DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).
 GN FLT4 OR FLT-4.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J;
 RX MEDLINE=9330572; PubMed=8393164;
 RA Finerty H., Kelleher K., Morris G.B., Bean K., Merberg D.M.,
 RA Kitz R., Morris J.C., Soekdeo H., Turner K.J., Wood C.R.,
 RT "Molecular cloning of murine FLT and FLT4".
 RL Oncogene 8:2293-2298(1993).
 CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
 CC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN
 CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.
 CC CSF-1/PDGF receptor subfamily.
 CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
 CC -----
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 CC -----
 DR EMBL: L07296; AAA0077.1; .
 DR PIR: I58375; I58375.
 DR HSP: P11362; IFGK.
 DR MGD: MGI:95561; Flt4.
 DR GO: GO:0005515; F: protein binding; IPI.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR007119; Prot_kinase.
 DR InterPro: IPR001824; ReceptcyrkinsIII.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR InterPro: IPR008266; Tyr_pkinase_AS.
 DR Pfam: PF00047; Ig_5.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 2.
 DR SMART: SM00408; IGc2; 2.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS50835; IG-LIKE; 5.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00101; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
 KW Glycoprotein.
 FT SIGNAL 1 24
 FT CHAIN 25 1363
 FT DOMAIN 25 775
 FT TRANSMEM 776 797
 FT DOMAIN 798 1363
 FT DOMAIN 44 118
 FT DOMAIN 151 213
 FT DOMAIN 230 326
 FT DOMAIN 331 415
 FT DOMAIN 422 552
 FT DOMAIN 555 671
 FT DOMAIN 678 764
 FT DOMAIN 845 1173
 FT NP_BIND 851 859
 FT BINDING 879 879
 FT ACT_SITE 1037 1037
 FT DISULFID 51 111
 FT DISULFID 158 206
 . VASCULAR ENDOTHELIAL GROWTH FACTOR
 . RECEPTOR 3.
 . EXTRACELLULAR (POTENTIAL).
 . POTENTIAL.
 . CYTOPLASMIC (POTENTIAL).
 . IG-LIKE C2-TYPE 1.
 . IG-LIKE C2-TYPE 2.
 . IG-LIKE C2-TYPE 3.
 . IG-LIKE C2-TYPE 4.
 . IG-LIKE C2-TYPE 5.
 . IG-LIKE C2-TYPE 6.
 . IG-LIKE C2-TYPE 7.
 . PROTEIN KINASE.
 . ATP (BY SIMILARITY).
 . ATP (BY SIMILARITY).
 . BY SIMILARITY.
 . POTENTIAL.
 . POTENTIAL.

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FT DISULFID 252 310 POTENTIAL.
FT DISULFID 445 534 POTENTIAL.
FT DISULFID 578 653 POTENTIAL.
FT DISULFID 699 751 POTENTIAL.
FT MOD RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1363 AA; 153015 MW; F1BFA2BDEF98B9 CRC64;

Query Match 7.3%; Score 95.5; DB 1; Length 1363;
Best Local Similarity 22.7%; Pred. No. 19;
Matches 42; Conservative 27; Mismatches 81; Indels 35; Gaps 6;

Oy 33 KQDTVELTCAQSKSIQPHMKNSNQIKIIGNQSS-----FLTKGPKLNDRAD 81
Db 570 EGGSVRLSCRDNDTYTHLRWRLNLSTLHDAQNPILLCKQVHLFATLEALNEBAEP 629
Oy 82 SRSRLDQGNFPLIKIKIEDSDTYICEVEDQKE-----VQLLVFGITANSDT 131
Db 630 GAR-----HATLSLNI PRVAPREDEDYCEVDRRSGQKHCKKYLVSQALFAPRLQNT 685
Oy 132 HLLGQGLTLESPPSS--PS-VQCRSPKKNIGG-----KTLVSQLELDQSGT 181
Db 686 DLVNVSDSLEMRCPVAGAHVPSIVWYKDRLEKESGIDPLADSNQRLSIQVREBDAGR 745
Oy 182 WTCVT 186
Db 746 YLCSV 750

RESULT 95
NEOL MOUSE STANDARD; PRT: 1493 AA.
ID NEOL MOUSE
AC P97798;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neogenin precursor.
GN NEOL OR NGN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RA MEDLINE=97407661; PubMed=9264410;
RX Keeling S.L., Gad J.M., Cooper H.M.;
RT "Mouse neogenin, a DCC-like molecule, has four splice variants and is
RT expressed widely in the adult mouse and during embryogenesis.";
RL Oncogene 15:691-700(1997).
CC -1- FUNCTION: May be involved as a regulatory protein in the
CC transition of undifferentiated proliferating cells to their
CC differentiated state. May also function as a cell adhesion
CC molecule in a broad spectrum of embryonic and adult tissues.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P97798-1; Sequence=Displayed;
CC Name=2;

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CC CC IsoId=P97798-2; Sequence=VSP_002594;
CC CC Name=3;
CC CC IsoId=P97798-3; Sequence=VSP_002595;
CC CC Note=Expression developmentally regulated;
CC CC Name=4;
CC CC IsoId=P97798-4; Sequence=VSP_002596;
CC CC Note=Expression developmentally regulated;
CC CC Name=5;
CC CC IsoId=P97798-5; Sequence=VSP_002597;
CC CC Note=Expression developmentally regulated;
CC CC -1- TISSUE SPECIFICITY: Widely expressed.
CC CC -1- DEVELOPMENTAL STAGE: EXPRESSED UBIQUITOUSLY THROUGHOUT THE MID TO
CC CC LATE STAGES OF GESTATION AND IN ADULT TISSUES. STRONG EXPRESSION
CC CC IS OBSERVED IN THE VENTRAL REGION OF THE VENTRICULAR ZONE OF THE
CC CC E15.5 MOUSE NEURAL TUBE, AS WELL AS IN THE VENTRICULAR ZONES OF
CC CC THE MESENCEPHALON AND RHOMBENCEPHALON. ISOFORMS 3 AND 4 ARE
CC CC EXPRESSED AT HIGHER LEVEL COMPARED TO OTHER ISOFORMS BETWEEN E11.5
CC CC AND E16.5.
CC CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily, DCC family.
CC CC -1- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC CC -1- SIMILARITY: Contains 6 fibronectin type III domains.
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC EMBL: Y09535; CAA70727.1; -.
CC CC HSSP: P02751; 1TTF.
DR MGD; MG1:1097159; Neol.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR007110; Ig_III-like.
DR InterPro: IPR003598; Ig_C2.
DR Pfam: PF00061; fn3; 6.
DR Pfam: PF00047; Ig; 4.
DR PRINTS: PR00014; ENTYPENIII.
DR SMART: SM00060; FN3; 6.
DR SMART: SM00408; IGC2; 4.
DR PROSITE: PSF0835; IG_LIKE_4.
DR Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW Glycoprotein; Alternative splicing.
FT SIGNAL 1 36
FT CHAIN 37 1493
FT FT 37 1136
FT DOMAIN 1137 1157
FT TRANSMEM 1158 1493
FT DOMAIN 63 158
FT DOMAIN 163 249
FT DOMAIN 254 347
FT DOMAIN 352 437
FT DOMAIN 467 564
FT DOMAIN 567 660
FT DOMAIN 661 760
FT DOMAIN 766 860
FT DOMAIN 881 981
FT DOMAIN 982 1083
FT DOMAIN 1149 1153
FT DISULFID 85 140
FT DISULFID 184 232
FT DISULFID 281 331
FT DISULFID 373 421
FT CARBOHYD 84 84
FT CARBOHYD 221 221
FT CARBOHYD 337 337
FT CARBOHYD 501 501
FT CARBOHYD 520 520
FT CARBOHYD 670 670
FT CARBOHYD 746 746

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FT CARBOHYD 940 940 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT VASPLIC 442 461 Missing (in isoform 2) .
FT VASPLIC 863 878 Missing (in isoform 3) .
FT VASPLIC 1086 1096 Missing (in isoform 4) .
FT VASPLIC 1279 1331 Missing (in isoform 5) .
FT VASPLIC 1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;
SEQUENCE 1493 AA; 163159 MW; 441DE919D5E17C0E CRC64;

Query Match 7.3%; Score 95.5; DB 1; Length 1493;
Best Local Similarity 25.0%; Pred. No. 21;
Matches 72; Conservative 29; Mismatches 94; Indels 93; Gaps 17;

QY 10 LVLVQLALPAA-----TQGNKV-----VLKGGDTVELT 40
DB 25 LLLLLPLLLGLRPAAGAAATKSGPRROGASVYTFPPFLVEPVDTLVRGGSVILN 84
QY 41 CTASQKSIQPHMKNSNIGKLGNGSFLTKGSKLNDRADSRSLMDQGNPILIKL 99
DB 85 CSAVSESPNIEWK-----KDGTF-----LNLESDDRQLPDSG--LFTSHV 126
QY 100 ----KIEBSPDYIC--EVED-----QKEVQLVFGI-----TANSDTHLQGSILTLLES 145
DB 127 HSKNNKPEGFYQCAYATDNGITVSRRAKLTVALPRFTQPESSVYVGNALNCEV 186
QY 146 PPGSSPSV---QCRSP-----RGKNIQGGKTLVSQLELQDSGTWC-----184
DB 187 NADLVPEFRWQGNQPLLDLRIVLPDSG--TLVISNATEGCGGLRCIVESGCPPKFSDE 245
QY 185 ---TYLQNKVKVEFRIDIV--PRASALPAPPGSALPPQPSALPDP 227
DB 246 AELKVLQDPEEI---VDLVFLMRPSM--MKVYTGQSAVLPCVSGSLPAP 289

RESULT 96
FCBL_RAT
ID FCBL_RAT STANDARD; PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FEER1) (IGF FC receptor, alpha-subunit) (Fc-epsilon RI-alpha) .
GN FCER1A OR FCER1A.
OS Rattus norvegicus (Rat) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RT "A cDNA presumptively coding for the alpha subunit of the receptor
RT with high affinity for immunoglobulin E." ;
RL Biochemistry 26:4605-4610(1987) .
RN (2)
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RP TISSUE=Test cells;
RX MEDLINE=88158102; PubMed=2964640;
RA Shimizu A., Tepler I., Bentley P.N., Berenstein E.H., Stragman R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products." ;
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988) .
RN (4)
RP SEQUENCE OF 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;

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RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IGE receptor." ;
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988) .
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -1- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two
CC DISULFIDE LINKED GAMMA CHAINS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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DR EMBL; M17153; AAA42045.1; -
DR EMBL; J03606; AAA41582.1; -
DR EMBL; M21622; AAA41146.1; -
DR PIR; G31327; A30154.
DR HSSP; P12319; IALS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 2.
DR SMART; SMO0409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 1.
KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT FT SIGNAL 1 23
FT CHAIN 1 245
FT FT
FT DOMAIN 24 204 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT TRANSMEM 205 223 RECEPTOR ALPHA-SUBUNIT.
FT DOMAIN 224 245 EXTRACELLULAR (POTENTIAL) .
FT DOMAIN 28 103 CYTOPLASMIC (POTENTIAL) .
FT DOMAIN 113 181 IG-LIKE 1.
FT DISULFID 49 91 IG-LIKE 2.
FT DISULFID 130 174 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 65 65 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL) .
SQ SEQUENCE 245 AA; 27793 MW; A0E67D363872197 CRC64;

Query Match 7.2%; Score 95; DB 1; Length 245;
Best Local Similarity 23.4%; Pred. No. 2.5;
Matches 50; Conservative 32; Mismatches 66; Indels 66; Gaps 10;

QY 11 LVLVQLALPAAATGNKRVLGK-----KQDTVELTC---TASQKSIQPHMKNSNOIKI 61
DB 13 LVLSISGLVMTATQKSVSLDPPWIRLTLDKVTLLGNGNNSQGMNSTK--WINDSI-- 68
QY 62 LGNGSFLTKGSKLNDRADSRSLMDQGNPILIKLKIEDSDTYICEVD--QKEVQ 119
DB 69 -----SNVKSISW-----YIVATITQDSGKYLCKQGFYKSRVY 103
QY 120 LVLVGLTANSDTHLQGSILTLTESPPGSSPSVQCGSPRG-----KNIQ 164
DB 104 LNVW-----QEWLLQSSADVLDN--GSPDRCRSMKKMKVKVITYKDDIAFKYSY 154
QY 165 GSKTLVSQLELQDSGTWCFTVLQNKVKVEFKID 198
DB 155 DSNNISIRKATFNDGSGYHCTGYLN--KVECKSD 186

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RESULT 97
 VGR2_HUMAN STANDARD; PRT; 1356 AA.
 ID VGR2_HUMAN STANDARD; PRT; 1356 AA.
 AC P35968; O60723; Q14178;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
 DE (VEGFR-2) (kinase insert domain receptor) (Protein-tyrosine kinase receptor Flk-1).
 DE KDR OR FLK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yin L.Y., Wu Y., Patterson C.;
 RT "Full length human KDR/Flk-1 sequence."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Umbilical vein;
 RA "Coding region for human VEGF receptor KDR (VEGFR-2)."
 RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 3-1356 FROM N.A.
 RC TISSUE=Umbilical vein;
 RA MEDLINE=92019839; PubMed=1656371;
 RX Terman B.I., Carrion M.E., Kovacs E., Rasmussen B.A., Eddy R.L.,
 RA Shows T.B.;
 RT "Identification of a new endothelial cell growth factor receptor
 tyrosine kinase."
 RL Oncogene 6:1677-1683(1991).
 RN [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=96032749; PubMed=7559454;
 RA Patterson C., Perrella M.A., Hsieh C.M., Yoshizumi M., Lee M.E.,
 RA Harber E.;
 RT "Cloning and functional analysis of the promoter for KDR/Flk-1, a
 receptor for vascular endothelial growth factor."
 RL J Biol. Chem. 270:23111-23118(1995).
 RN [5]
 RP FUNCTION:
 RX MEDLINE=93038639; PubMed=1417831;
 RA Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D.,
 RA Armellino D.C., Gospodarowicz D., Boehlen P.;
 RT "Identification of the KDR tyrosine kinase as a receptor for vascular
 endothelial cell growth factor."
 RL Biochem. Biophys. Res. Commun. 187:1579-1586(1992).
 CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
 KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
 PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
 VASCULAR PERMEABILITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.
 CC CSF-1/PDGF receptor subfamily.
 CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
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 CC -----
 DR EMBL; AF035121; AAB88005.1; -.

DR EMBL; AF063658; AAC16450.1; -.
 DR EMBL; X61656; CAA43837.1; -.
 DR EMBL; L04947; CAA59459.1; -.
 DR EMBL; X89776; CAA61916.1; -.
 DR PIR; JCI402; JCI402.
 DR HSSP; P11362; 1FGK.
 DR Genew; HGNC:6307; KDR.
 DR MIM; 191306; -.
 DR GO; GO:0005887; C.integral to plasma membrane; TAS.
 DR GO; GO:0005021; F.vascular endothelial growth factor receptor. . .; TAS.
 DR GO; GO:0007169; P.transmembrane receptor protein tyrosine kin. . .; TAS.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_C2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR01824; RecepttyrkinaIII.
 DR InterPro; IPR01245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF00047; Ig_6.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 2.
 DR SMART; SM00408; IgC2; 2.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
 DR Angiogenesis; Signal; Transferase; Tyrosine-protein kinase; Receptor;
 KW Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.
 KW Immunoglobulin domain; Repeat.
 KM CHAIN 1 19
 FT 20 1356
 FT DOMAIN 20 764
 FT TRANSMEM 765 789
 FT DOMAIN 790 1356
 FT DOMAIN 46 110
 FT DOMAIN 141 207
 FT DOMAIN 224 320
 FT DOMAIN 328 414
 FT DOMAIN 421 548
 FT DOMAIN 551 660
 FT DOMAIN 667 753
 FT DOMAIN 834 1162
 FT NP BIND 840 848
 FT BINDING 868 868
 FT ACT SITE 1028 1028
 FT CARBOHYD 46 46
 FT CARBOHYD 66 66
 FT CARBOHYD 96 96
 FT CARBOHYD 143 143
 FT CARBOHYD 158 158
 FT CARBOHYD 245 245
 FT CARBOHYD 318 318
 FT CARBOHYD 374 374
 FT CARBOHYD 395 395
 FT CARBOHYD 511 511
 FT CARBOHYD 523 523
 FT CARBOHYD 523 523
 FT CARBOHYD 580 580
 FT CARBOHYD 613 613
 FT CARBOHYD 619 619
 FT CARBOHYD 631 631
 FT CARBOHYD 675 704
 FT CARBOHYD 704 721
 FT CARBOHYD 721 1059
 FT MOD RES 1059 1059
 FT CONFLICT 2 2
 FT CONFLICT 772 772
 FT CONFLICT 787 787
 FT CONFLICT 835 835
 FT CONFLICT 848 848
 FT CONFLICT 1347 1347
 SO SEQUENCE 1356 AA; 151526 MM; 59E7C44B05CEBB3 CRC64;

Page : 1

Query Match Similarity 7.2%; Score 94.5; DB 1, Length 108, 3,
Pred. No 0.99; 53; Indels 9; Gaps 3,
Best local similarity 33.0%; 7; Mismatches 82
Matches 34; Conservative

CG TGGKRVYAGKKDPTVETCTASQKRSIQHWNKSNOIKLGNQSGFLTKGSPKLNRAQS 60
DB 23 : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
5 TQPSLSISVGDKNVTITCOASODISIFLWVGOKP---SKAPKLIVADSKLEAVPS 60
CG 83 RRLIMDOG-NFPLILKLIKEDSDTYICEVEPDKEEVLVLFG 124
DB 61 RFSGTGSGLDTFFTLSSLOPEDIRATTCQDPNLP---LTFG 99

RESULT 99
CD8B-PONPY STANDARD: PRT: 210 AA.

CD8B-PONPY
AC P30434; (Rel. 25, Created)
AC 01-APR-1993 (Rel. 25, Last sequence update)
DC 10-OCT-2003 (Rel. 42, Last annotation update)
DR 10-OCT-2003 (Rel. 42, Last annotation update)
DR 10-OCT-2003 (Rel. 42, Last annotation update)
DR T-cell surface glycoprotein CD8 beta chain precursor;
DR CD8B.
GR Pongo pygmaeus (Orangutan).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euarchontomi;
OC Mammalia; Primates; Catarrhini; Homnidae; Pongo.
NCBI_Taxid=9600;

[1]
SEQUENCE FROM N.A.
RP STRAIN=Isolate Jari; PubMed=1612644;
RC MEDLINE=92307742; Parham P.;
RX Lawlor D.A. of CD8 alpha and beta chains of the orangutan:
RT "structure of mRNA splicing encoding hingedless polypeptides";
RT patterns of mRNA splicing cytochrome c/suppressor T-cells that interact in
RU immunogenesis identifies cytotoxic/cd8 is thought co play a role in
RL -1- FUNCTION: Identifies cytotoxic/cd8 is thought co play a role in
RL with MHC class I bearing targets.
CC the process of T-cell-mediated killing.
CC -1- SUBUNIT: In general disulfide bonds.
CC linked by two disulfide bonds.
CC -1- SUBUNIT: In general disulfide bonds.
CC linked by two disulfide bonds.
CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Comment: A number of isoforms are produced. Alternative splicing
CC involves excision of the hinge or cytoplasmic domains.
CC Name=1; Sequence=Displayed;
CC IsoId=P30434-1; Immunoglobulin-like V-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit statement is not removed. See http://www.isb-sb.ch/announce
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CC or send an email to license@isb-sb.ch).

EMBL: X60222; CMA2783.1; -
CC FIRM: S25657; S25657.
DR PIR: S25657; C.T-cell receptor complex; ISS.
DR GO: GO:0042101; C.T-cell receptor activity; ISS.
DR GO: GO:0042105; F:coreceptor binding; ISS.
DR GO: GO:0015088; F:MHC class binding; ISS.
DR GO: GO:0005255; F:immune response; ISS.
DR GO: GO:0006950; P:T-cell activation; ISS.
DR GO: GO:0042169; P:T-cell activator protein tyrosine kin. . ; ISS.
DR GO: GO:0007189; P:transmembrane receptor protein tyrosine kin. . ; ISS.
DR Interpro: IPRO03599; IG-like.
DR Interpro: IPRO03599; IG-like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00485; IG_LIKE_1.
DR PROSITE: PS50985; Transmembrane; T-cell; Antigen; Glycoprotein.
DR Immunoglobulin domain; Transmembrane; T-cell; Antigen; Glycoprotein.
KM Immune response; Signal; Alternative splicing.
BY SIMILARITY.
21
F1 SIGNAL

```
FT CHAIN 22 210 T-CELL SURFACE GLYCOPROTEIN CD8 BETA
FT DOMAIN 22 170 CHAIN
FT TRANSMEM 171 191 EXTRACELLULAR (POTENTIAL)
FT DOMAIN 192 210 POTENTIAL
FT DOMAIN 22 123 CYTOPLASMIC (POTENTIAL)
FT DISULFID 41 116 IG-LIKE V-TYPE
SQ SEQUENCE 210 AA; 23693 MW; F455B0F281C73DC1 CRC64;

Query Match 7.2%; Score 94.5; DB 1; Length 210;
Best Local Similarity 25.7%; Pred. No. 2.2;
Matches 45; Conservative 23; Mismatches 72; Indels 35; Gaps 8;

QY 10 LLLVQLALL-----PA--ATGKNVYLCKGDTVLTCTAS-QKKSIFHKNS 57
DB 7 LLLAQLAVHGGSSVLOQTDAVYKVNKKVM-----LSCAKISNNMRYLRR 58
QY 58 QIKILGNGSFL-----TKGPSKLNDRADRSRLM-DQGNFPLIKLKIEDSDTYICEV 111
DB 59 QARSSDHEHFLALMDAKTIISEVEQKAVFRASFLINLSVKEDSGIFYCWI 118
QY 112 EDOKEVQLVFGLTANSSTHLLQGSLTLTSSPPGSSPSVQ-CNSPRKNIQG 165
DB 119 VGSPE-----LTFGKGTQLSVDFLPTTAOPTKSTPKRRVCRLPRPETOKG 165

RESULT 100
BUTY_MOUSE STANDARD; PRT; 524 AA.
ID BUTY_MOUSE
AC Q62556; P97392;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Butyrophilin precursor (BT) (Butyrophilin subfamily 1 member A1).
GN BTN1A1 OR BTN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Mammary gland;
RX MEDLINE=97148936; Pubmed=8995761;
RA Ogg S.L., Komargiri M.V.S., Mather I.H.;
RT "Structural organization and mammary-specific expression of the
RT butyrophilin gene."
RL Mamm. Genome 7:900-905(1996).
RN (2)
RP SEQUENCE OF 39-487 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=96125722; Pubmed=8541302;
RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.;
RT "Carboxy-terminal cytoplasmic domain of mouse butyrophilin
RT specifically associates with a 150-kDa protein of mammary epithelial
RT cells and milk fat globule membrane."
RL Biochim. Biophys. Acta 1245:285-292(1995).
CC -!- FUNCTION: May function in the secretion of milk-fat droplets. It
CC may act as a specific membrane-associated receptor for the
CC association of cytoplasmic droplets with the apical plasma
CC membrane (By similarity).
CC -!- SUBUNIT: Seems to associate with xanthine dehydrogenase/oxidase.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in mammary tissue and secreted in
CC association with the milk-fat-globule membrane during lactation.
CC -!- DEVELOPMENTAL STAGE: Expression increases during the last half of
CC pregnancy and is maximal during lactation.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. BTN/MOG
CC family.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC -----
CC EMBL; U67065; AAB51034.1; -.
CC EMBL; S80642; AAB35893.1; -.
CC MGD; MG1:103118; Bttnal.
DR InterPro; IPR001870; B302.
DR InterPro; IPR007110; IG-V.
DR InterPro; IPR003596; IG-V.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00042; SPRY_1.
DR Pfam; PF00622; SPRY_1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00589; PRY; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50835; IG_LIKE_2.
KM Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
FT SIGNAL 1 36
FT CHAIN 27 524
FT DOMAIN 27 247
FT TRANSMEM 248 268
FT DOMAIN 269 524
FT DOMAIN 29 141
FT DOMAIN 149 235
FT CARBOHYD 36 56
FT CARBOHYD 216 216
FT CONFLICT 46 46
FT CONFLICT 117 117
FT CONFLICT 191 191
FT CONFLICT 210 210
FT CONFLICT 363 363
FT CONFLICT 408 408
FT CONFLICT 413 414
FT CONFLICT 420 423
FT CONFLICT 492 509
SQ SEQUENCE 524 AA; 58406 MW; 333F4DE2C7704480 CRC64;

Query Match 7.2%; Score 94.5; DB 1; Length 524;
Best Local Similarity 22.3%; Pred. No. 6.9;
Matches 62; Conservative 42; Mismatches 99; Indels 75; Gaps 13;

QY 11 LVLQLALLPAA-----TGANKVYLCKGDTVLTCTASQKSIQF---HKNSQIQT 61
DB 16 LTVLQLPTLDSAAPDVTAPQEPVVALVGSDELTCGFSPNASSSEYMWELWFRQTRSTAV 75
QY 62 L-----GNQGSFLT--KGPSKLNDRADRSRLMDQGNFPLIKLKIEDSDTYICEVED 113
DB 76 LLYRDQDEQEGQOMTEYRGRAFL-----ATAGLLD-GRATLLRDVAVDQGEYRLCLFED 129
QY 114 ---QKEVQLVFGLTANSSTHLLQGSLTLTSSPPGSSPSVQCRS----- 157
DB 130 NDDFEAAVYLVKAAVAGSPQISMVTEGEMELCTSSGWYPEPQVQRTGNREMLPST 189
QY 158 --PRGKNIGKTLVSQLELDG--TWTCIV---LONQKVEKDIIVPAASALPAP 209
DB 190 SESEKNEBGLFVAVSNM-IRDSISKNSCCIONILLQOGKEVEI----- 234
QY 210 PTGSALPDPTASALPDPAASALPALAVISFLGLG 247
DB 235 -----SLPAPVPRVLTPIVAIILLALG 259

Search completed: August 3, 2004, 13:09:18
Job time : 7.54316 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 12:51:44 ; Search time 17.7158 Seconds
(without alignments)
4594.975 Million cell updates/sec

Title: SEQ6
Perfect score: 1317
Sequence: 1 MNRGVPRRLHLVLQALLP.....VISFLGLGIVACVLARTR 258

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database :
1: SPREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767	58.2	397	6	009261 cercoptithec
2	767	58.2	397	6	009262 cercoptithec
3	767	58.2	397	6	009263 cercoptithec
4	767	58.2	397	6	009264 cercoptithec
5	763	57.9	397	6	009259 cercoptithec
6	763	57.9	397	6	009260 cercoptithec
7	758	57.6	397	6	002805 cercoptithec
8	741.5	56.3	457	6	08H2T8 calilitrix
9	740.5	56.2	457	6	08H2T7 calilitrix
10	592	45.0	455	6	09X5T8 delphinapte
11	557.5	42.3	474	6	061355 felis alive
12	467	35.5	457	11	061356 mus musculu
13	436.5	33.1	433	11	055054 mus musculu
14	400	30.4	86	6	077596 mandrillus
15	400	30.4	86	6	077597 mandrillus
16	397	30.1	86	6	077594 cercoptithec

17	397	30.1	86	6	077599 theropithec
18	395	30.0	86	6	077595 cercocebus
19	392	29.8	86	6	077598 papio sp. (
20	388	29.5	86	6	077601 lophocebus
21	383	29.1	86	6	077600 lophocebus
22	357	27.1	71	4	013969 homo sapien
23	305.5	23.2	99	6	029027 sus scrofa
24	280.5	21.3	99	6	029028 sus scrofa
25	172	13.1	482	13	090WB5 anas platytr
26	157.5	12.0	538	6	029123 sus scrofa
27	156.5	11.9	538	6	028939 sus scrofa
28	153	11.6	487	13	09W6V7 gallus gall
29	144	10.9	287	11	09D7B8 gallus gall
30	141	10.7	650	6	09GKR2 mus musculu
31	141	10.7	739	6	09GKR3 mus musculu
32	132	10.0	739	6	028260 canis famli
33	131.5	10.0	1496	4	092626 homo sapien
34	131	9.9	955	4	08NFP4 homip4 homo sapien
35	130	9.9	338	4	08IV49 homo sapien
36	130	9.9	1259	11	090Y38 mus musculu
37	129.5	9.8	437	4	081ZP8 homo sapien
38	129	9.8	731	6	08SP16 aspie macropus eu
39	126	9.6	341	11	08BLK3 mus musculu
40	125.5	9.5	226	4	013857 homo sapien
41	125.5	9.5	1431	11	080U60 mus musculu
42	125	9.5	332	4	08TA95 homo sapien
43	125	9.5	358	13	08UV81 brachydanio
44	125	9.5	390	4	09HIX9 homo sapien
45	125	9.5	512	4	096DN8 homo sapien
46	125	9.5	545	5	09VCT4 drosophila
47	125	9.5	5636	4	096RW7 homo sapien
48	124.5	9.5	394	11	09EOK9 ratius norv
49	124.5	9.5	504	13	098823 gallus gall
50	124.5	9.5	584	13	098821 gallus gall
51	124.5	9.5	584	13	090989 gallus gall
52	124.5	9.5	626	13	098922 gallus gall
53	124.5	9.5	626	13	090880 gallus gall
54	124.5	9.5	2828	4	09NRP9 homo sapien
55	124	9.4	325	13	08UV52 brachydanio
56	124	9.4	739	11	063669 ratius norv
57	122.5	9.3	532	5	09VLE0 drosophila
58	122	9.3	355	4	0723B1 hom sapien
59	122	9.3	1009	13	093250 xenopus lae
60	121	9.2	885	6	08HYV1 sus scrofa
61	121	9.2	886	6	08HY2 sus scrofa
62	120	9.1	1005	13	P79921 xenopus lae
63	120	9.1	1091	11	P70193 mus musculu
64	120	9.1	2222	5	097394 drosophila
65	119.5	9.1	311	11	09JLM2 ratius norv
66	119	9.0	352	13	09W6V2 gallus gall
67	119	9.0	1395	5	044924 drosophila
68	118.5	9.0	276	13	08AW79 brachydanio
69	118.5	9.0	278	13	08AW80 brachydanio
70	118.5	9.0	584	4	09Y3Y8 homo sapien
71	118	9.0	348	11	080Z24 mus musculu
72	118	9.0	403	5	09VP08 drosophila
73	118	9.0	577	11	09D221 mus musculu
74	118	9.0	577	11	080Y42 mus musculu
75	118	9.0	1395	5	09W213 drosophila
76	118	9.0	4117	5	08IRV9 drosophila
77	118	9.0	4179	5	09W4Y4 drosophila
78	118	9.0	4223	5	08MPV3 drosophila
79	118	9.0	6831	5	023550 caenorhabdi
80	118	9.0	7158	5	023551 caenorhabdi
81	117	8.9	350	7	002869 gallus gall
82	117	8.9	811	5	09VNP2 drosophila
83	117	8.9	1011	5	024273 drosophila
84	116.5	8.8	192	11	07TQ03 mus musculu
85	116.5	8.8	285	4	043608 homo sapien
86	116.5	8.8	359	5	09V6C2 drosophila
87	116.5	8.8	570	4	08NCE6 homo sapien
88	116.5	8.8	660	4	072681 homo sapien
89	116.5	8.8	739	6	0865F2 oryctolagus

Db 121 GSSPSVCKRSPRGKNIQGRITLSPQLERODSGTWTCTVSODONTVEFKIDIV 173

RESULT 3

ID 009263 PRELIMINARY; PRT; 397 AA.

AC 009263;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE CD4 (Fragment).

GN CD4.

OS Cercopithecus tantalus.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OC NCBI_TaxId=60712;

CK (1)

RN SEQUENCE FROM N.A.

RP MEDLINE=98017879; PubMed=9379478;

RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S., "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes.";

RT J. Med. Primatol. 26:120-128(1997).

RL EMBL; AF001222; AAB60869.1; -.

DR HSSP; P01730; 1WIO.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000973; CD4_TcAg.

DR InterPro; IPR007110; Ig_Like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_2.

DR PRINTS; PR00692; CD4TCANTIGEN.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1 1

FT SEQUENCE 397 AA; 43994 MW; A3CD01535A51524 CRC64;

SO

Query Match 58.2%; Score 767; DB 6; Length 397;

Best Local Similarity 85.5%; Pred. No. 1.2e-58;

Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Db 28 VLAKKGDVLTCTASQKSIQPHMKNSQIKILNGSFLTGPKLNDRAISRSLW 87

1 VLAKKGDVLTCTASQKSIQPHMKNSQIKILNGSFLTGPKLNDRAISRSLW 60

Qy 88 DQGNFPLIINKLKIEDSDTYICEVEDQKEVQLVFGLTANSPTHLQOGSLTTLSP 147

61 DQGFMSIINKLKIEDSETYICEVENKEEVELLVFGLTANSPTHLQOGSLTTLSP 120

Db 148 GSSPSVCKRSPRGKNIQGRITLSPQLERODSGTWTCTVSODONTVEFKIDIV 200

121 GSSPSVCKRSPRGKNIQGRITLSPQLERODSGTWTCTVSODONTVEFKIDIV 173

Db

RESULT 4

ID 009259 PRELIMINARY; PRT; 397 AA.

AC 009259;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE CD4 (Fragment).

GN CD4.

OS Cercopithecus pygerythrus.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OC NCBI_TaxId=60710;

CK (1)

RN SEQUENCE FROM N.A.

RP

EX MEDLINE=98017879; PubMed=9379478;

RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S., "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes.";

RT J. Med. Primatol. 26:120-128(1997).

RL EMBL; AF001227; AAB60874.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000973; CD4_TcAg.

DR InterPro; IPR007110; Ig_Like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_2.

DR PRINTS; PR00692; CD4TCANTIGEN.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1 1

FT SEQUENCE 397 AA; 43946 MW; 21C3E30882ABFC0 CRC64;

SO

Query Match 58.2%; Score 767; DB 6; Length 397;

Best Local Similarity 85.5%; Pred. No. 1.2e-58;

Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Db 28 VLAKKGDVLTCTASQKSIQPHMKNSQIKILNGSFLTGPKLNDRAISRSLW 87

1 VLAKKGDVLTCTASQKSIQPHMKNSQIKILNGSFLTGPKLNDRAISRSLW 60

Qy 88 DQGNFPLIINKLKIEDSDTYICEVEDQKEVQLVFGLTANSPTHLQOGSLTTLSP 147

61 DQGFMSIINKLKIEDSETYICEVENKEEVELLVFGLTANSPTHLQOGSLTTLSP 120

Db 148 GSSPSVCKRSPRGKNIQGRITLSPQLERODSGTWTCTVSODONTVEFKIDIV 200

121 GSSPSVCKRSPRGKNIQGRITLSPQLERODSGTWTCTVSODONTVEFKIDIV 173

Db

RESULT 5

ID 009259 PRELIMINARY; PRT; 397 AA.

AC 009259;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE CD4 (Fragment).

GN CD4.

OS Cercopithecus sabaesus.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Cercopithecus.

OC NCBI_TaxId=60711;

CK (1)

RN SEQUENCE FROM N.A.

RP MEDLINE=98017879; PubMed=9379478;

RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S., "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes.";

RT J. Med. Primatol. 26:120-128(1997).

RL EMBL; AF001223; AAB60870.1; -.

DR HSSP; P01730; 1WIO.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR000973; CD4_TcAg.

DR InterPro; IPR007110; Ig_Like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig_2.

DR PRINTS; PR00692; CD4TCANTIGEN.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1 1

FT SEQUENCE 397 AA; 43881 MW; 7CE39AD0F8506C81 CRC64;

SO

Query Match 57.9%; Score 763; DB 6; Length 397;
Best Local Similarity 85.0%; Pred. No. 2.6e-58;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGDVLTCTASOKSIOPHMKNNOIKILGQSFLLKGPCKLNDRADSRSLW 87
DB 1 VVLGKGDVLTCTASOKSIOPHMKNNOIKILGQSFLLKGPCKLNDRADSRSLW 60

QY 88 DQGNFPLIKNLKIEDSDTYICEVEDQKEEVOLLVFGLTANSPTHLLOQGSLLTLESPP 147
DB 61 DQGFSSMIKNLKIEDSETYICEVENKEEVEVLVFGLTANSPTHLLOQGSLLTLESPP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQKKEVFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQKKEVFKIDIV 173

RESULT 6
ID 009260 PRELIMINARY; PRT; 397 AA.
AC 009260;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE CD4 (Fragment).
GN CD4.
OS Cercopithecus sabaesus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60711;
RN [1]
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001224; AAB60871.1; -.
DR HSSP; P01730; IWIO.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR003596; Ig_Like.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_Like; 1.
FT NON_TER 1
FT SEQUENCE 397 AA; 43882 MW; 478BB277E92EE89 CRC64;
SQ

Query Match 57.9%; Score 763; DB 6; Length 397;
Best Local Similarity 85.0%; Pred. No. 2.6e-58;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGDVLTCTASOKSIOPHMKNNOIKILGQSFLLKGPCKLNDRADSRSLW 87
DB 1 VVLGKGDVLTCTASOKSIOPHMKNNOIKILGQSFLLKGPCKLNDRADSRSLW 60

QY 88 DQGNFPLIKNLKIEDSDTYICEVEDQKEEVOLLVFGLTANSPTHLLOQGSLLTLESPP 147
DB 61 DQGFSSMIKNLKIEDSETYICEVENKEEVEVLVFGLTANSPTHLLOQGSLLTLESPP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQKKEVFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDSGTWTCTVLOQKKEVFKIDIV 173

RESULT 7

002805
ID 002805 PRELIMINARY; PRT; 397 AA.
AC 002805; 077593;
DT 01-JUL-1997 (TREMblrel. 04, Created)
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3) (Fragment).
GN CD4.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA Corbet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
RN [2]
RX MEDLINE=98320644; PubMed=9656488;
RA Harris B.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (Primates: Papionini).";
ML Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 3 C2-LIKE DOMAINS.
DR EMBL; AF001226; AAB60873.1; -.
DR EMBL; AF057380; AAC25124.1; -.
DR HSSP; P01730; IWIO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_Like.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
KM Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KM Lipoprotein; Palmitate; Repeat.
FT NON_TER 1
FT DOMAIN <1 370
FT TRANSMEM 371 391
FT DOMAIN 392 >397
FT DOMAIN <1 98
FT DOMAIN 99 176
FT DOMAIN 177 290
FT DOMAIN 291 347
FT CARBOHYD 15 15
FT CARBOHYD 30 30
FT CARBOHYD 269 269
FT CARBOHYD 298 298
FT DISULFID 14 82
FT DISULFID 128 157
FT DISULFID 301 343
FT LIPID 392 392
FT LIPID 395 395
FT NON_TER 397 397
SQ SEQUENCE 397 AA; 43980 MW; F74C42E22B196155 CRC64;
Query Match 57.6%; Score 758; DB 6; Length 397;
Best Local Similarity 85.0%; Pred. No. 7.1e-58;
Matches 147; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

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Qy 28 VLAKKGGDTVELTASQKSIQFHMKNISNOIKILGNQGSFLTCKSPKLNDRADSRSLW 87
Db 1 VVLGKGGDTVELTASQKSIQFHMKNISNOIKILGNQGSFLTCKSPKLNDRADSRSLW 60
Qy 88 DQGNFPLIIKNIKIEDSDTYICEVDOKEVQLVFGLTANSPTLLQGSLLTLESPP 147
Db 61 DQGNFPLIIKNIKIEDSDTYICEVDOKEVQLVFGLTANSPTLLQGSLLTLESPP 120
Qy 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTCTVVLQNKKEFKIDIV 200
Db 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTCTVVLQNKKEFKIDIV 173

RESULT 8
Q8H278 PRELIMINARY; PRT; 457 AA.
AC Q8H278;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Lymphocyte antigen CD4.
OS Calitrix jaccus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
OX NCBI_Taxid=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22174698; PubMed=12186836;
RX Labonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World Monkey Cells Occurs
RT Primarily at the Stage of Virus Entry."
RL J. Exp. Med. 196;431-445(2002).
DR EMBL; AF452616; AAN14532.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000973; CD4_TCAG.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 457 AA; 50878 MW; 718CFDB78D97F59B CRC64;

Query Match 56.3%; Score 741.5; DB 6; Length 457;
Best Local Similarity 72.5%; Pred. No. 2.4e-56;
Matches 145; Conservative 23; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MNRGVPFRHLLVQLALLPAATGKNVYLCKGDTVELTASQKSIQFHMKNISNOIK 60
Db 1 MNRGVPFRHLLVQLALLPAATGKNVYLCKGDTVELTASQKSIQFHMKNISNOIK 60
Qy 61 ILGNQGSFLTCKSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDOKEVQL 120
Db 61 ILGNQGSFLTCKSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDOKEVQL 120
Qy 121 LVFGLTANSPTLLQGSLLTLESPPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
Db 121 LVFGLTANSPTLLQGSLLTLESPPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
Qy 121 QVFGLTANPDTLLQGSLLTLESPPSSPSVECSPRGKIRGRKTLVSQIGIPDSG 180
Db 121 QVFGLTANPDTLLQGSLLTLESPPSSPSVECSPRGKIRGRKTLVSQIGIPDSG 180
Qy 181 TWCTCTVLQNKKEFKIDIV 200
Db 181 TWCTCTVLQNKKEFKIDIV 199

RESULT 9
Q8H277 PRELIMINARY; PRT; 457 AA.
AC Q8H277;
DT 01-MAR-2003 (Tremblrel. 23, Created)

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DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Lymphocyte antigen CD4.
OS Salimiri beirurus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_Taxid=9521;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22174698; PubMed=12186836;
RX Labonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World Monkey Cells Occurs
RT Primarily at the Stage of Virus Entry."
RL J. Exp. Med. 196;431-445(2002).
DR EMBL; AF452617; AAN14533.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000973; CD4_TCAG.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 457 AA; 50899 MW; B164DA89F70C575A CRC64;

Query Match 56.2%; Score 740.5; DB 6; Length 457;
Best Local Similarity 72.0%; Pred. No. 2.9e-56;
Matches 144; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

Qy 1 MNRGVPFRHLLVQLALLPAATGKNVYLCKGDTVELTASQKSIQFHMKNISNOIK 60
Db 1 MNRGVPFRHLLVQLALLPAATGKNVYLCKGDTVELTASQKSIQFHMKNISNOIK 60
Qy 61 ILGNQGSFLTCKSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDOKEVQL 120
Db 61 ILGNQGSFLTCKSPKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVDOKEVQL 120
Qy 121 LVFGLTANSPTLLQGSLLTLESPPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
Db 121 LVFGLTANSPTLLQGSLLTLESPPSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
Qy 121 QVFGLTANPDTLLQGSLLTLESPPSSPSVECSPRGKIRGRKTLVSQIGIPDSG 180
Db 121 QVFGLTANPDTLLQGSLLTLESPPSSPSVECSPRGKIRGRKTLVSQIGIPDSG 180
Qy 181 TWCTCTVLQNKKEFKIDIV 200
Db 181 TWCTCTVLQNKKEFKIDIV 199

RESULT 10
Q9XS78 PRELIMINARY; PRT; 455 AA.
AC Q9XS78;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_Taxid=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Thymus;
RX MEDLINE=99216435; PubMed=10199913;
RA Romano T.A., Ridgway S.H., Felten D.L., Quaranta V.;
RT "Molecular cloning and characterization of CD4 in an aquatic mammal,
RT the white whale Delphinapterus leucas."
RL Immunogenetics 49;376-383(1999).
DR EMBL; AF071179; AAD23738.1; -.
DR HSP; P01730; IWO.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO: GO:0006955; P:Immune response; IEA.
DR InterPro: IPR000973; CD4 TcAg.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00692; CD4TcANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR SEQUENCE 455 AA; 50499 MW; AA532PD411AA5D1 CRC64;

Query Match 45.0%; Score 592; DB 6; Length 455;
Best Local Similarity 60.0%; Pred. No. 2.7e-43;
Matches 120; Conservative 24; Mismatches 56; Indels 0; Gaps 0;

OY 1 MNRGVPFHLILLYQLALLPATQGNKVVLLKKKGDVTLCTASOKKSIOEHMKNQNIK 60
DB 1 MDPRSLRHLFLVLDVWMLPAGTQKKVVLGKAGELABLCKASQNSLFFSMKNSYOTK 60
OY 61 ILGNQSFLLTKGPSKLANDRADSRRLMDQGNFPLIKNLKIEDSPYICVEDQKEEVQL 120
DB 61 ILGRHGVFMWKGASVLRHSVESKILMLDQGSFPLVTKDLEVPDGGTYICEVDKKIEVEL 120
OY 121 LVFLGASDPHLLOGSGLTTLTSPSSSSVQCRSRGNIGQSGKTLVSQLELDQSG 180
DB 121 QVFRITASSDPRLLLGOSLTTLTEGSSNPSSVQMGKGNRKNEAKSLSLPVELDQSG 180
OY 181 TWCTCTVLQNKQKVEFKIDIV 200
DB 181 TWCTCTVSAQQTIVENKHIL 200

RESULT 11
P79355 PRELIMINARY; PRT; 474 AA.
ID P79355
AC P79355
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD4 antigen precursor.
OS Fells silvestris cactus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazawa T.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92165316; PubMed=1537604;
RA Notimite J., Miyazawa T., Kawaguchi Y., Tohya Y., Kai C., Mikami T.;
RT "A CDNA encoding feline CD4 has a unique repeat sequence downstream of
RT the V-like region."
RL Immunology 75:74-79(1992).
DR EMBL; AB000483; BAA19124.1; -.
DR HSSP: P01730; 1WIO.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0006955; P:Immune response; IEA.
DR InterPro: IPR000973; CD4 TcAg.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_3.
DR PRINTS: PR00692; CD4TcANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS50835; IG_LIKE; 2.
KW Signal.
FT SIGNAL 1 26
FT CHAIN 27 474 POTENTIAL.
SQ SEQUENCE 474 AA; 52243 MW; D946DD4BEAED0EC CRC64;

Query Match 42.3%; Score 557.5; DB 6; Length 474;
Best Local Similarity 55.3%; Pred. No. 3e-40;
Matches 121; Conservative 30; Mismatches 49; Indels 19; Gaps 3

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Oy	I	MNRGVPFRHLLVLTOTALLPAAAT--QGNKVVLGGKGGTVELTCTASOKKSIOFHMKNSNOI	59
Dd	1	MNQGAVFRHLLLVQLVWLAKAAPPQKEVVLAGAGTAELPCQASQKKITFTWRILSSQV	60
Oy	60	KIIIGNGSFFL-TGPSKTLNDRADRSRLMDQGNFPIIKNLKIEDSPDTYICEVEDOKEEV	118
Dd	61	KIIESGHSSSLCLTGSSSLTKRPFESKKIIMDQGSFPLVYSKLQVADSGLTYCEVENKREY	120
Oy	119	QLVFGLTANS-----THLIQGSYLTTLESPPSSSVOCRSFRGK	161
Dd	121	ELLVFGILTAYKVDPSGGSGSSSTSTSTSYLLQGSOLTTLESPPSSSNPSVQMGPGNK	180
Oy	162	NIOGGKTLVSOLEIODSGTWTCIVLONOKVEFKDIIV	200
Dd	181	SKGVSHLSLSQLEBLQESGTCTCTVSOXKTIVFNINIL	219

RESULT 12

ID	O61396	PRELIMINARY;	PRT;	457 AA.
AC	O61396,			
DT	01-NOV-1996 (TREMBLrel_01, Created)			
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel_25, last annotation update)			
DE	T-cell differentiation antigen.			
CN	CD4.			
CS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=86041153; Pubmed=2823269;			
RA	Gorman S.D., Tourville B., Parnes J.R.;			
RT	"Structure of the mouse gene encoding CD4 and an unusual transcript in			
RT	brain."			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).			
DR	EMBL; M17080; AAA37402.1; -			
DR	EMBL; M17076; AAA37402.1; JOINED.			
DR	EMBL; M17077; AAA37402.1; JOINED.			
DR	EMBL; M17078; AAA37402.1; JOINED.			
DR	EMBL; M17079; AAA37402.1; JOINED.			
DR	HSSP; P01730; IMBR.			
DR	MGP; MG1:88335; Cd4.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR000973; CD4_TC4g.			
DR	InterPro; IPR007110; Ig_V.			
DR	Pfam; PF00047; Ig; 2.			
DR	PRINTS; PR00692; CD4TCANTIGEN.			
DR	SMART; SMO0406; Igy; 1			
DR	PROSITE; PS50835; Ig_Like; 1.			
SQ	SEQUENCE 457 AA; 51368 MW; 24AB19EDA285B5D0 CRC64;			

Query Match	35.5%; Score 467; DB 11; Length 457;
Best Local Similarity	52.3%; Pred. No. 2,3e-33;
Matches 103; Conservative	32; Mismatches 56; Indels 6; Gaps 5;

Oy	1	MNRGVPFRH-LLVLTOTALPAATQGNKVVLGGKGDTEVELTCTASOKKSIOFHMKNSNOI	59
Dd	1	MCRAISIRLRILLLLQLQSLLAVTQEFTLYLGKGESAELPCBESSQKKITFTWKFSDOR	60
Oy	60	KIIENOG-SFLTRG--TSKLNDRADRSRLMDQGNFPIIKNLKIESDPDYICEVEPOKE	116
Dd	61	KIILOHGEGVILRGSSSPQ--DRPDSKKGAWEKSFPIINKLMEDSQTYICLENKE	119
Oy	117	EVQLVVGELTPANSTPHLLQGSILTTLES--PGSSPVQCRRSPGRKNIOGKTVSVQLE	175
Dd	120	EVELMVRKVTPTSPETSIILQGSLLTLTDNSNKSYNPLTECHKRKGKYVSSGKVLMSMYLR	179
Oy	176	LQDSGVTCTIVLQNOKK	192

Db 180 VQSDSFNCTVTLDDCK 196

RESULT 13

055054 PRELIMINARY; PRT; 433 AA.

AC 055054; (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE T4 surface glycoprotein (Fragment).
 GN CD4.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RX MEDLINE=88097446; PubMed=3501122;

RA Maddon P.J., Molineux S.M., Maddon D.E., Zimmerman K.A., Godfrey M.,

Alt F.W., Chees U., Axel R.;

"Structure and expression of the human and mouse T4 genes.";

Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159 (1987).

RP SEQUENCE FROM N.A.

RA Maddon P.J., Molineux S.M., Maddon D.E., Zimmerman K.A., Godfrey M.,

Alt F.W., Chees U., Axel R.;

Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF045882; AAC01764.1; -.

DR HSSP; P01730; 1MBR.

DR MGD; MGI:88335; CD4.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR000973; CD4_TCSG.

DR InterPro; IPR007110; IG_Like.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF00047; Ig_2.

DR PRINTS; PRO00692; CD4TCANTIGEN.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON TER 1

FT NON TER 433

SO SEQUENCE 433 AA; 48590 MW; AB19330750A8499A CRC64;

Query Match 33.1%; Score 436.5; DB 11; Length 433;

Best Local Similarity 53.2%; Pred. No. 9.9e-30;

Matches 92; Conservative 29; Mismatches 47; Indels 5; Gaps 4;

QY 24 QGNKVVIGKGDYELTCTASQKSIOPHMKNSNQIKLGNQ-SFLTKG--PSKNDRA 80

DB 1 QGKTLVIGKEGSESLPESSQKITTPTWKFSDRKTLGHGKGVLRGSPSQF-DRF 59

QY 81 DSRSLMDQGNFPLIKLKIEDSDTYCEVEDQKEEVLVFGLTANSPTHLQGGSLT 140

DB 60 DSKGAMKGSFPLINKLKIEDSTYICELNKEKEVLEWVFVKTSPGSLQGGSLT 119

QY 141 LTLES-PPGSSPSVQCRSPRGKNIQGGKTLISVSOLELDSGTWTCTVQLQNGK 192

DB 120 LTLDSNKKVSNPLTECKHKKGVSGKVLMSNLRVQSDPFNCTVTLDDCK 172

RESULT 14

077596 PRELIMINARY; PRT; 86 AA.

AC 077596; (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)

OS Mandrillus sphinx (Mandrill).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

CC Cercopithecoidea; Mandrillus.

NX NCBI_TaxID=9561;

RP SEQUENCE FROM N.A.

RX MEDLINE=98320644; PubMed=9656488;

RA Harris B.E., Diotcell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the

mangabey (primates: Papionini)."

Mol. Biol. Evol. 15:892-900 (1998).

-1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL

RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY

SIMILARITY).

-1- SUBUNIT: ASSOCIATES WITH PS6-LCK (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

ONE V-LIKE AND 1 C2-LIKE DOMAIN.

DR EMBL; AF057386; AAC25130.1; -.

DR HSSP; P01730; 1CDY.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR InterPro; IPR007110; IG_Like.

DR Immunoglobulin domain; T-cell; MHC; Transmembrane.

FT NON TER 1

FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.

FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.

FT DISULFD 49 78 BY SIMILARITY.

FT NON TER 86 86

SO SEQUENCE 86 AA; 9406 MW; 2BD97A9EB19582AB CRC64;

Query Match 30.4%; Score 400; DB 6; Length 86;

Best Local Similarity 89.4%; Pred. No. 1.9e-27;

Matches 76; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVLVFGLTANSPTHLQGGSLTLLESPPGSSPSVQCRSPRGKNIQGG 166

DB 1 YICEVEDQKEEVLVFGLTANSPTHLQGGSLTLLESPPGSSPSVQCRSPRGKNIQGG 60

QY 167 KTLISVSOLELDSGTWTCTVQLQNGK 191

DB 61 KTLISVPOLELDSGTWTCTVQSDCK 85

RESULT 15

077597 PRELIMINARY; PRT; 86 AA.

AC 077597; (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)

OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

CC Cercopithecoidea; Mandrillus.

NX NCBI_TaxID=9568;

RP SEQUENCE FROM N.A.

RX MEDLINE=98320644; PubMed=9656488;

RA Harris B.E., Diotcell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the

mangabey (primates: Papionini)."

Mol. Biol. Evol. 15:892-900 (1998).

-1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL

RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY

SIMILARITY).

-1- SUBUNIT: ASSOCIATES WITH PS6-LCK (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

ONE V-LIKE AND 1 C2-LIKE DOMAIN.

DR EMBL; AF057387; AAC25131.1; -.

DR HSSP; P01730; 1CDY.

DR GO; GO:0016021; C:Integral to membrane; IEA.

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DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT NON TER 49 78 BY SIMILARITY.
SQ SEQUENCE 86 AA; 9406 MW; 2BD97A9EE19582AB CRC64;

Query Match 30.4%; Score 400; DB 6; Length 86;
Best Local Similarity 89.4%; Pred. No. 1.9e-27;
Matches 76; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLTGQSLTLTLESPGSSPSVQCKSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLTGQSLTLTLESPGSSPSVKCRSPRGKNIQGG 60
QY 167 KTLVSQLELDGSGTWTCTVNLQOK 191
DB 61 KTLSPQLERODSGTWTCTVNSQDOK 85

RESULT 16
ID 077594 PRELIMINARY; PRT; 86 AA.
AC 077594;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus mitis.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36225;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT NON TER 49 78 BY SIMILARITY.
SQ SEQUENCE 86 AA; 9420 MW; 2BD97A98574EB9AB CRC64;

Query Match 30.1%; Score 397; DB 6; Length 86;
Best Local Similarity 88.2%; Pred. No. 3.4e-27;
Matches 75; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLTGQSLTLTLESPGSSPSVQCKSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLTGQSLTLTLESPGSSPSVKCRSPRGKNIQGG 60
QY 167 KTLVSQLELDGSGTWTCTVNLQOK 191
DB 61 KTLSPQLERODSGTWTCTVNSQDOK 85

RESULT 17
ID 077599 PRELIMINARY; PRT; 86 AA.
AC 077599;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disocell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR007110; Ig-like.
KW Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT NON TER 49 78 BY SIMILARITY.
SQ SEQUENCE 86 AA; 9420 MW; 2BD97A98574EB9AB CRC64;

Query Match 30.1%; Score 397; DB 6; Length 86;
Best Local Similarity 88.2%; Pred. No. 3.4e-27;
Matches 75; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 107 YICEVEDQKEEVQLVFGLTANSPTHLTGQSLTLTLESPGSSPSVQCKSPRGKNIQGG 166
DB 1 YICEVEDKKEVELVFGLTANSPTHLTGQSLTLTLESPGSSPSVKCRSPRGKNIQGG 60
QY 167 KTLVSQLELDGSGTWTCTVNLQOK 191
DB 61 KTLSPQLERODSGTWTCTVNSQDOK 85

RESULT 18
ID 077595 PRELIMINARY; PRT; 86 AA.
AC 077595;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus galatellus chrysogaster.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=75569;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disocell T.R.;
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RESULT 17
ID 077599 PRELIMINARY; PRT; 86 AA.
AC 077599;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disocell T.R.;

RESULT 18
ID 077595 PRELIMINARY; PRT; 86 AA.
AC 077595;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
OS (Fragment).
OC Cercopithecus galatellus chrysogaster.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=75569;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disocell T.R.;
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RT "Nuclear gene trees and the phylogenetic relationships of the
RL mangabey (primates: Papionini)."
CC MoJ. Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR EMBL; AF057382; AAC25126.1; -.
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007110; Ig-like.
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT NON_TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 49 78 BY SIMILARITY.
FT SEQUENCE 86 86
SQ SEQUENCE 86 AA; 9419 MW; A9D97A9EE19582BE CRC64;

Query Match 30.0%; Score 395; DB 6; Length 86;
Best Local Similarity 88.2%; Pred. No. 5,1e-27;
Matches 75; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 107 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTLTLESPGSSPSVQCSPRGKNIQGG 166
DB 1 YICEVEDKKEVELLVGLTNSDTHLLLEGSLTLTLESPGSSPSVQCSPRGKNIQGG 60
QY 167 KTLVSQLELDSDGTWCTVYQONOK 191
DB 61 RTLSVPOLERQDSGTWCTVNSQDOK 85

RESULT 19
QY 077598 PRELIMINARY; PRT; 86 AA.
AC 077598;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE (Fragment).
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
CX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disotell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RL MoJ. Biol. Evol. 15:892-900(1998)."
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR EMBL; AF057388; AAC25132.1; -.
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007110; Ig-like.
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT NON_TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFD 49 78 BY SIMILARITY.
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9463 MW; 2BD97A88464FB3AB CRC64;

Query Match 29.5%; Score 388; DB 6; Length 86;
Best Local Similarity 87.1%; Pred. No. 2,1e-26;
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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FT DISULFD 49 78 BY SIMILARITY.
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9433 MW; A9D97A9857AEE3BE CRC64;

Query Match 29.8%; Score 392; DB 6; Length 86;
Best Local Similarity 87.1%; Pred. No. 9,3e-27;
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 107 YICEVEDQKEVQLLVGLTNSDTHLLQGSLTLTLESPGSSPSVQCSPRGKNIQGG 166
DB 1 YICEVEDKKEVELLVGLTNSDTHLLLEGSLTLTLESPGSSPSVQCSPRGKNIQGG 60
QY 167 KTLVSQLELDSDGTWCTVYQONOK 191
DB 61 RTLSVPOLERQDSGTWCTVNSQDOK 85

RESULT 20
QY 077601 PRELIMINARY; PRT; 86 AA.
AC 077601;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/LEU-3)
DE (Fragment).
OS Lophocebus albigena albigena.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Lophocebus.
CX NCBI_TaxID=75568;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; Pubmed=9656488;
RA Harris E.E., Disotell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RL MoJ. Biol. Evol. 15:892-900(1998)."
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR EMBL; AF057391; AAC25135.1; -.
DR HSSP; P01730; 1CDY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR007110; Ig-like.
KM Immunoglobulin domain; T-cell; MHC; Transmembrane.
FT NON_TER 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT CARBOHYD 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT DISULFD 49 78 BY SIMILARITY.
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9463 MW; 2BD97A88464FB3AB CRC64;

Query Match 29.5%; Score 388; DB 6; Length 86;
Best Local Similarity 87.1%; Pred. No. 2,1e-26;
Matches 74; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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AC 077600;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE (Fragment).
OS Lophocobus aeterinus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Lophocobus.
OC NCBI_TaxID=75566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris E.E., Disotell T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the
RT mangabeys (primates: Papionini).";
RL Mol. Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
CC SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE AND 1 C2-LIKE DOMAIN.
DR EMBL; AF057390; AAC25134.1.; -
DR HSSP; P01730; ICDY.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR007110; Ig-like.
KM Immunoglobulin domain; Glycoprotein; T-cell; MHC; Transmembrane.
FT NON_TER 1 1
FT DOMAIN <1 19 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 20 >86 IG-LIKE C2-TYPE DOMAIN.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 49 78 BY SIMILARITY.
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9476 MW; A9D97A88464FE9BE CRC64;

Query Match 29.1%; Score 383; DB 6; Length 86;
Best Local Similarity 85.9%; Pred. No. 5,7e-26;
Matches 73; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 107 YICEVEQKEVQLVFGFLTANSPDTHLLOGSLTLTLESPGSSPVQCRSPKKNIOG 166
DB 1 YICEVEKKEVELLVGFLTANSTHLLBEGSLTLTLESPGSSPVQCRSPKKNIOG 60
QY 167 KTLVSQLELDQSGTWTCTVLQNOCK 191
DB 61 RTLSPQLERQDSGTWTCNVSDQCK 85

RESULT 22
Q13969 PRELIMINARY; PRT; 71 AA.
AC Q13969;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CD4 protein (Fragment).
DE CD4.
GN CD4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zverev V.V., Blinov V.M., Nedospasov S.A.;
RT "Splice-mediated insertion of antisense Alu repeats in human
RT CD4 gene: identification of three exons of CD4 mRNA.";
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95407135; PubMed=7676667;

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RA Zverev V.V., Sidorov A.V., Nedospasov S.A., Malushova V.V.,
RA Udajova I.A., Andzhaparidze O.G., Blinov V.M.;
RT "Nucleotide sequence of two exons of the human T-lymphocyte CD4
RT receptor gene.";
RL Vopr. Virusol. 40:100-102(1995).
RL EMBL; X87579; CAA60883.1.; -
DR EMBL; S79267; AAB35273.1.; -
DR PIR; I60082; I60082.
DR HSSP; P01730; ICDY.
DR GO; GO:0004872; F: receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Receptor.
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 7844 MW; A5C9D84816135C86 CRC64;

Query Match 27.1%; Score 357; DB 4; Length 71;
Best Local Similarity 98.6%; Pred. No. 8,3e-24;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVFRLVLVQLALPAPATQGNKYVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
DB 1 MNRGVFRLVLVQLALPAPATQGNKYVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
QY 61 ILGNQGSFLLTK 71
DB 61 ILGNQGSFLLTK 71

RESULT 23
Q29027 PRELIMINARY; PRT; 99 AA.
AC Q29027;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CD4, allele 1 (Fragment).
DE CD4, allele 1 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H183; TISSUE=Blood;
RX MEDLINE=93329116; PubMed=8335933;
RA Gustafsson K., Germania S., Sundt T.M., Sachs D.H., Leguenn C.;
RT "Extensive allelic polymorphism in an exposed region of the
RT minature. . .";
RL J. Immunol. 151:1365-1370(1993).
DR EMBL; X65629; CAA46583.1.; -
DR PIR; I47131; S21461.
DR HSSP; P01730; ICDY.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR PIR; PFO0047; IG_V.
DR SMART; SM00406; IG_V; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 11170 MW; 40BF080699CF5DOC CRC64;

Query Match 23.2%; Score 305.5; DB 6; Length 99;
Best Local Similarity 60.2%; Pred. No. 4e-19;
Matches 59; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

QY 32 KKGDVVELTCTASQKKSIOFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADRSRLWDG 90
DB 1 KAGDLALDELPHSSQKKNLPFNWKNSTQTKILGSGHGFMTASTVLTSLRSLDKKNWMDHG 60
QY 91 NPLLIITKLKIEDSDTYICEVEQKEVQLLVGLTAN 128
DB 61 SFLIITKLKLEVTDSGIYICEVEDKRIEVLVLRITAS 98

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RESULT 24
Q29028      PRELIMINARY;      PRT;      99 AA.
ID   Q29028
AC   Q29028;
DT   01-NOV-1996 (TREMBlrel. 01, Created)
DT   01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT   01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE   CD4, allele 2 (Fragment).
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX   NCBI_Taxid=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN#1183; TISSUE=Blood;
RA   MEDLINE=93329116; PubMed=8335933;
RA   Gustafsson K., Germana S., Sundt T.M., Sachs D.H., Leguern C.;
RT   "Extensive allelic polymorphism in an exposed region of the
RT   major histocompatibility complex (MHC) class II gene region in
RL   J. Immunol. 151:1365-1370(1993).
DR   EMBL; X65630; CAA46584.1; -.
DR   PIR; I47332; S21462.
DR   HSSP; P01730; ICDY.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_V.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IgV_1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1
FT   NON_TER      99
FT   NON_TER      99
SQ   SEQUENCE 99 AA; 11390 MW; C22955E8A228318F CRC64;

Query Match      21.3%; Score 280.5; DB 6; Length 99;
Best Local Similarity 56.1%; Pred. No. 6.2e-17;
Matches 55; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

QY 32 KKGDVLTCTASQKSIQFHWKNSNQIKILGNQGSFLTKCP-SKLNDRADRSRLMDQG 90
DB 1 KAGGLAEIPCHSSQKQKLPFSWKNSDQIKIRSHRNLMHKASVTELSRLDSKKMMDHG 60
QY 91 NFPLIINKLIKIEDSDTYICEVEDQKEEYQVLVFGITAN 128
DB 61 GFPLIKLEVTDSGIYCEVEDKRIEYQLVFLRTAS 98

RESULT 25
Q290WBS      PRELIMINARY;      PRT;      482 AA.
ID   Q290WBS
AC   Q290WBS;
DT   01-DEC-2001 (TREMBlrel. 19, Created)
DT   01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT   01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE   T-cell surface glycoprotein CD4 precursor.
OS   Anas platyrhynchos (Domestic duck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinoptera; Anseriformes; Anatidae; Anas.
CX   NCBI_Taxid=8839;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Chan S.W.S., Middleton D.L., Lundqvist M., Marr G.W., Higgins D.A.;
RA   Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF318701; AAK59279.1; -.
DR   InterPro; IPR003599; IG.
DR   InterPro; IPR007110; IG-like.
DR   Pfam; PF00047; Ig_4.
DR   SMART; SM00409; IG_3.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Signal.
FT   SIGNAL      1
FT   SIGNAL      29
SQ   SEQUENCE 482 AA; 54624 MW; BDA08BEC6172AD0B CRC64;
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Query Match      13.1%; Score 172; DB 13; Length 482;
Best Local Similarity 25.7%; Pred. No. 1.5e-06;
Matches 57; Conservative 41; Mismatches 76; Indels 48; Gaps 9;

QY 8 RHLLVQLALPPATQGNKVLGKGDVLTCTASQKSIQFHWK-----NSNQIK 60
DB 12 RAVFVLLQGLV--THIMAHQOQIVGEGKEVILNC---KKHDKQVTKVEYDAGSSAIIIQ 66
QY 61 ILGNQGSFLTKGPKANDRADRSRLMDQGNFPLIINKLIKIEDSDTYICEVEDQKEEYQVL 120
DB 67 ILACK---IFKGRAPMSDRSET-----NQNSKHLKVNLRISDAGTYICEGSDRNISL 118
QY 121 LVFGLTANSPDTHILQGGSLTIT--LESPGSSPS-----VQCSPPKKN 162
DB 119 HVVLTITSSNGVFLPGDDELITVHKSPKSPRSTITLFSNRSRVPEVLQNETPQ--- 175
QY 163 IGGKTLISVQLKQSDSGTWTCTVLQN---QKKVEEKIDIV 200
DB 176 ---KYALKVKQLQPTDSGTWICNNHSDSPSINENISFVKVL 214

RESULT 26
Q29123      PRELIMINARY;      PRT;      538 AA.
ID   Q29123
AC   Q29123;
DT   01-NOV-1996 (TREMBlrel. 01, Created)
DT   01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT   01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE   Vascular cell adhesion molecule.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX   NCBI_Taxid=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RA   MEDLINE=94271236; PubMed=7516159;
RA   Tsang Y.T., Haskard D.O., Robinson M.K.;
RT   "Cloning and expression kinetics of porcine vascular cell adhesion
RT   molecule.";
RL   Biochem. Biophys. Res. Commun. 201:805-812(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aorta;
RC   MEDLINE=96106491; PubMed=8525525;
RA   Mueller J.P., Evans M.J., Coffell R., Rother R.P., Matis L.A.,
RA   Elliott B.A.;
RT   "Porcine vascular cell adhesion molecule (VCAM) mediates endothelial
RT   cell adhesion to human T cells. Development of blocking antibodies
RT   specific for porcine VCAM.";
RL   Transplantation 60:1299-1306(1995).
DR   EMBL; L43124; AAB59281.1; -.
DR   HSSP; P19320; IVCA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0016337; P:cell-cell adhesion; IEA.
DR   InterPro; IPR003987; ICAM_VCAM-1.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003598; IG_c2.
DR   InterPro; IPR003989; VCAM-1.
DR   Pfam; PF00047; Ig_5.
DR   PRINTS; PR01472; ICAMVCAM1.
DR   PRINTS; PR01474; VCAM1.
DR   SMART; SM00408; IGC2; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain.
SQ   SEQUENCE 538 AA; 58713 MW; 8A7CD36D0A2F0717 CRC64;

Query Match      12.0%; Score 157.5; DB 6; Length 538;
Best Local Similarity 25.0%; Pred. No. 3.2e-05;
Matches 50; Conservative 38; Mismatches 71; Indels 41; Gaps 6;

QY 32 KKGDVLTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPKANDRADRSRLMDQGN 91
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Db      235 QEDGSVMWMTCTSGCLAPQISW-----SKKDNGDQQL---SGN 271
Qy      92 FPLIINKLKIEDSDTYICE---VEDQKEVQLV-----FGLTANSDTHLLQGSULT 141
Db      272 ATLTLTAMRMEDSGIYCEGVNPGVTRKEVELTVQAPRDTTISVNPSTLEGGSSVM 331
Qy      142 TLESPPGSSPSV---QCRSPRGNKIQGKTLVSQLELDGSGTWCTVLQ---NOKKY 193
Db      332 TCSSDGPAPKILMSKRLRDNLEPSENTTLTLTSTKMEDSGIYVCDGINQGINRKEY 391
Qy      194 EFKIDIVPRASALPAPPTGS 213
Db      392 ELIIQAPKDLQTLAPSES 411

RESULT 27
ID Q28939 PRELIMINARY; PRT; 538 AA.
AC Q28939;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Vascular cell adhesion molecule precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RX REFSEQ: Sequence from N.A.
RC MEDLINE=94271236; PubMed=7516159;
RA Trang Y.T., Haekard D.O., Robinson M.K.;
RT "Cloning and expression kinetics of porcine vascular cell adhesion
RL molecule."
RL EMBL; U08351; AAA21542.1; -.
DR PIR; JC2457; JC2457.
DR HSP; P19320; 1YCA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003987; ICAM VCAM-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003988; Ig C2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; Ig_5.
DR PRINTS; PRO1472; ICAMVCAM1.
DR SMART; SM00408; IGc2_3.
DR PROSITE; PS50835; IG_LIKE; 4.
KM Immunoglobulin domain; Signal.
FT SIGNAL 1 24
FT CHAIN 25 538 VASCULAR CELL ADHESION MOLECULE.
SQ SEQUENCE 538 AA; 58795 MW; EC29D11B224F7261 CRC64;

Query Match 11.9%; Score 156.5; DB 6; Length 538;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;
Matches 49; Conservative 39; Mismatches 71; Indels 41; Gaps 6;

Qy      32 KKGDYVELCTASQKSIQFHWKNSNQIKLGNQSFITKPSKLNDRADRSRLMDQGN 91
Db      235 QEDGSVMWMTCTSGCLAPQISW-----SKKDNGDQQL---SGN 271
Qy      92 FPLIINKLKIEDSDTYICE---VEDQKEVQLV-----FGLTANSDTHLLQGSULT 141
Db      272 ATLTLTAMRMEDSGIYCEGVNPGVTRKEVELTVQAPRDTTISVNPSTLEGGSSVM 331
Qy      142 TLESPPGSSPSV---QCRSPRGNKIQGKTLVSQLELDGSGTWCTVLQ---NOKKY 193
Db      332 TCSSDGPAPKILMSKRLRDNLEPSENTTLTLTSTKMEDSGIYVCDGINQGINRKEY 391
Qy      194 EFKIDIVPRASALPAPPTGS 213

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Db      392 ELIIQAPKDLQTLAPSES 411

RESULT 28
ID Q96V7 PRELIMINARY; PRT; 487 AA.
AC Q96V7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE CD4 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX REFSEQ: Sequence from N.A.
RC STRAIN=H.B2; TISSUE=Thymus;
RA Koskinen R.H., Salomonsen J., Tregaskes C.A., Young J.R.,
RA Goodchild M., Bumstead N., Vainio O.;
RT "The chicken CD4 gene has remained conserved in evolution."
RL Immunogenetics 0:0-0(2002).
DR EMBL; Y12012; CAA72740.1; -.
DR EMBL; A0401223; CAC82027.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_3.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Signal.
FT SIGNAL 1 28
FT CHAIN 29 487 VASCULAR CELL ADHESION MOLECULE.
SQ SEQUENCE 487 AA; 54985 MW; B9CBA92EC9F7F45B CRC64;

Query Match 11.6%; Score 153; DB 13; Length 487;
Best Local Similarity 27.8%; Pred. No. 6.9e-05;
Matches 59; Conservative 28; Mismatches 87; Indels 38; Gaps 8;

Qy      10 LLLVQLALPAAATGKAVLGGKPTVELTCTA-SQKSIQFHWKNSNQIKLGNQSFITKPSKLNDRADRSRLMDQGN 91
Db      14 VILVQLGLTLPMAQEQOI-GIAGKEVILSCAINNQDGTCTWKYKYSSTIISFS 72
Qy      64 NGGSFITKPSKLNDRADRSRLMDQGNFPLIINKLKIEDSDTYICEVEDQKEVQLV 123
Db      73 KAVFEGKAPM-----THRELSNNSKKLVSDLSDDAGIYTACACSPVVISLHVF 125
Qy      124 GLTANSDTHLLQGSULTL-ESPSSPS-----VOCSPRGNKIQG 165
Db      126 KLTISNGHPLTMEDELTLQNSSHSPHLSTKLFNINNDIYTTELDEARQ-KYI-- 182
Qy      166 GKTLVSQLELDGSGTWCTVLQNKVKEFKI 197
Db      183 ---LKLKQKALDSDGTMCHVYNSPSINQNI 211

RESULT 29
ID Q9D7B8 PRELIMINARY; PRT; 287 AA.
AC Q9D7B8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 2310016B05Rik protein.
DE D1ERTD736E OR 2310016B05RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Akawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kaakawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Maceno Y., Nakado I., Pesele G., Quackenbush J.,
RA Schriml L.M., Strubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Boujanga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gutentich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohlschki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009375; BAB26251.1; -
DR MGI; MGI:1289168; D11Etd736e.
DR InterPro; IPR003599; 1g_1.
DR InterPro; IPR007110; 1g_1like.
DR Pfam; PF00047; 1g_1.
DR SMART; SM00409; 1g_1.
DR PROSITE; PS50835; 1g_LIKE; 1.
SQ SEQUENCE 287 AA; 32061 MW; D9324D3308A03639 CRC64;

Query Match 10.9%; Score 144; DB 11; Length 287;
Best Local Similarity 23.0%; Pred. No. 0.00021;
Matches 68; Conservative 46; Mismatches 110; Indels 72; Gaps 11;

QY 8 RHLLVQLALPA--ATGKKNVVGKGGTVELTCTASOK-KSIQFWKNSNOIK--- 60
DB 2 RPLVLMGCLVLPGEALKEKKEISGFEQDTVSLCTVEVKEKHKRYKCRQGILVSR 61
QY 61 ---ILNGSGFLTGKPSKLNDRADSRSLMDQGNFLLIKLKIEDSDTYICEV---D 113
DB 62 GDIYVANDQEVTRKMSIR---DSPQL---SFTVIMRLDTLKDSKVCYCGIDRLGRD 114
QY 114 QKEEVQLLVF-----GLTNSDTHLQSGSLTLTSSPGSSPSVOCRSP---R 159
DB 115 ESFEVTLVFPGSYRPVWMLPTTPQDS-----RAVASVSKPSVISIMVMMAVLI 169
QY 160 GKNIQGGKTLVSQLELDSGTWTCTVLQONKVEFK-----IDIVPRA 203
DB 170 SLILAAGIAGSHMLRWKKAMLATEQKNKLVLETSPLNGWTTEDSTIDLAVPEEC 229
QY 204 -----SLPAPPT---GSALPDPTASALPD-----PRAASLPAALAVISFL 243
DB 230 LRNIINPAPVPEPTONISQSTEEBAARSLLDDKEDVNAAPPLOMSAEELAFSEPT 285

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RESULT 30

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QY 09GKR2 PRELIMINARY; PRT; 650 AA.
AC 09GKR2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Vascular cell adhesion molecule-1 6D variant lacking D7 precursor.
GN VCA1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Muscle;
RA Muroya S., Nakajima I., Chikuni K.;
RT "Novel alternative splicing variant of bovine vascular cell adhesion molecule-1."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052747; BAB19782.1; -
DR HSSP; P19320; 1VCA.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR Pfam; PF00047; 1g_6.
DR SMART; SM00408; 1g_c2; 2.
DR PROSITE; PS50835; 1g_LIKE; 4.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 24
FT CHAIN 25 650
FT VASCULAR CELL ADHESION MOLECULE-1 6D VARIANT LACKING D7.
SQ SEQUENCE 650 AA; 71821 MW; 24244573EF255E40 CRC64;

Query Match 10.7%; Score 141; DB 6; Length 650;
Best Local Similarity 25.6%; Pred. No. 0.0011;
Matches 52; Conservative 35; Mismatches 60; Indels 56; Gaps 10;

QY 32 KKQDTVELTCTASOKKSIQFWKNSNOIKILNGSGFLTGKPSKLNDRADSRSLMDQGN 91
DB 238 QEGDSVMTCTASAGLPAPRILMS-----KKL-----DNGN 267
QY 92 FPLIKN-----LKIEDSDTYICE--VEDQKEVQLV-----FGLTNSDTHLQ- 135
DB 268 RQLSENATLTLIRWADSGIYCEGNPVGKREKVLTVGKNFTVEISPPQIAAQ 327
QY 136 -GQSLTLTLESPPSSPSVOCR---SPRGKNI--QSGK-TLSVSOLELDSGTWTCTVL 187
DB 328 VGDSIVLTCVPRDCESSFSFWRILIDSPPLNGVNSSEKSTLTLSPVSEHFHYLCTVM 387
QY 188 QNOKKVEFKIDIVPRASALPAP 210
DB 388 CGQKKLEKRIQVXP--YSPSPNP 408

RESULT 31
QY 09GKR3 PRELIMINARY; PRT; 739 AA.
AC 09GKR3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Vascular cell adhesion molecule-1 7D variant precursor.
GN VCA1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Muscle;
RA Muroya S., Nakajima I., Chikuni K.;
RT "Novel alternative splicing variant of bovine vascular cell adhesion molecule-1."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB052746; BAB19650.1; -
DR HSSP; P19320; 1VCA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003987; ICAM_VCAM-1.
DR InterPro; IPR007110; 1g_1like.
DR InterPro; IPR003598; 1g_c2.
DR InterPro; IPR003989; VCA1-1.
DR Pfam; PF00047; 1g_7.

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	SQ	SEQUENCE	739 AA;	81398 MW;	CA32EJ141117AIBF CRC64;	POTENTIAL. VASCULAR CELL ADHESION MOLECULE-1 7D VARIANT.
DR	PRINTS;PR01472;	ICAMVCAM1.				
DR	PRINTS; PR01474;	ICAMVCAM1.				
DR	SMART; SMO0408;	IGC2; 3				
DR	PROSITE; PS50835;	IG_LIKE; 5.				
KW	Immunoglobulin domain;	Signal.				
FT	SIGNAL	1	24			
FT	CHAIN	25	739			
Query Match						
Best Local Similarity		10.7%; Score 141;	DB 6;	Length 739;		
Matches	52; Conservative	25.6%; Pred. No. 0.0013;	Mismatches 60;	Indels 56;	Gaps 10;	
OY	32 KKGDVTVELCTASQKKSIOFHKK--NSNQIKILGNQSFLTKGPSKLNDRAISRSLMD	91				
Dd	238 QEGSVMTCSAGAPARILMS-----DKL-----DNEN	267				
Oy	92 PPLIKN-----LKIEDSPTYCE---VEDOKEVOVLIV---PGLTANSDTHLIQ-	135				
Dd	268 RQLSENATLTLLISMRADSGIYCEGNNPVGRKEVKTLTVOEKNFVEISPGEIJAAQ	327				
Oy	136 -GSSTLTLESPPSSPSPOCR---SPRGKI--GGK-TLSVSQLEDSGTWTCHYL	187				
Dd	328 VEDSVTLCDVRDCESPFSFWTTLDISPLNGVNRSSEGSTLTUSPVSFEHHFYLCVM	387				
Oy	188 QNOKVFEEKIDIVPPRASALPAPE 210					
Dd	388 CGQKLEKRGIQKP--YSFPNP 408					
RESULT 32						
ID	Q28260	PRELIMINARY;	PRT;	739 AA.		
AC	Q28260;					
DT	01-NOV-1996 (TREMBRel. 01. Created)					
DT	01-NOV-1996 (TREMBRel. 01. Last sequence update)					
DI	01-OCT-2003 (TREMBRel. 25. Last annotation update)					
DE	Vascular cell adhesion molecule-1.					
OS	Caris familiaris (Dog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC	Mammalia; Euteria; Carnivora; Fissipedia; Canidae; Canis.					
OX	NCHI_Taxid=9615;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Ballantyne C.M., Clubb F.J., Perrard J.L., Radovencovic B.,					
RA	Youker K.A., Smith C.W., Entman M.L., Hawkins H.K., Frazier O.H.,					
RA	"Increased Expression of VCAM-1 and ICAM-1 in Early Cardiac Allograft					
RT	Arteriopathy in the Dog";					
RL	Submitted (Jul-1995) to the EMBL/genbank/DDBJ databases.					
DR	HMBL; U32086; AAA84866.1; .					
DR	HSBP; PI9320; IVCA.					
DR	GO; GO:0016020; C:membrane; IEA.					
DR	GO; GO:0016337; P:cell-cell adhesion; IEA.					
DR	IInterPro; IPR003987; ICAM VCAM-1.					
DR	IInterPro; IPR007110; Ig-like.					
DR	IInterPro; IPR003598; IG_C2.					
DR	Ifam; PF00047; Ig; 7.					
DR	PRINTS; PR01472; ICAMVCAM1.					
DR	PRINTS; PR01474; VCAM1.					
DR	SMART; SMO0408; IGC2; 4.					
DR	PROSITE; PS50835; IG_LIKE; 5.					
KM	Immunoglobulin domain.					
SQ	SEQUENCE 739 AA; 81412 MW; BB5DA3853739C615 CRC64;					
Query Match						
Best Local Similarity		10.0%; Score 132;	DB 6;	Length 739;		
Matches	47; Conservative	24.7%; Pred. No. 0.0082;	Mismatches 60;	Indels 48;	Gaps 9;	
OY	32 KKGDVTVELCTASQKKSIOFHKK--NSNQIKILGNQSFLTKGPSKLNDRAISRSLMD	88				

ID	Q92626	PRELIMINARY:	PRT:	1496 AA.
Qy	89	OGNFFPLINKLIEHSDPYIC-----EVEDQKEEYQVLLY----	FGLTANSDPHLLQ--	GOS 138
Db	271	SGNATLTLLNMLEEISGVTCVEGVNEVKQKQGEVLLVQEKPFVLEISPGQIIAQIGDS		330
Qy	139	LTVLTLESPGSSPS-----VQCRSPRG--KNIQGK-TLSVSOQLDQSGTWTCTVLQNOK		191
Db	331	VVLTCGVTDCEPSFSWRQIDSLGSGTVKEGAKSTLTLSPVLENEHSYLCVTTCGCHK		390
Qy	192	KVE--FKIDI 199		
Db	391	KLEKGIKVDL 400		
RESULT 33				
ID	Q92626	PRELIMINARY:	PRT:	1496 AA.
AC	Q92626;			
DT	01-FEB-1997 (TrEMBLrel. 02, Created)			
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)			
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	MYELOBLAST KIA0230 (Fragment).			
GN	KIAA0230.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone marrow;			
RC	MEDLINE=97191344; PubMed=9039502;			
RA	Nagaee T., Seki N., Ishikawa K., Ohira M., Kawarabayashi Y., Ohara O.,			
RA	Tanaka A., Kotani H., Miyajima N., Nomura N.;			
RT	"Prediction of the coding sequences of unidentified human genes. VI.			
RT	The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by			
RT	analysis of cDNA clones from cell line KG-1 and brain.";			
RL	DNA Rep. 3:321-329(1996).			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RC	MEDLINE=95048383; PubMed=7959781;			
RA	Weller S.R., Taylor S.M., Deans R.J., Kan-Mitchell J., Mitchell M.S.,			
RA	Trent J.M.;			
RT	"Assignment of a human melanoma associated gene M650 (D2S448) to			
RT	chromosome 2p25.3 by fluorescence in situ hybridization.";			
RL	Genomics 22:243-244(1994).			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanoma;			
RC	Mitchell M.S., Kan-Mitchell J., Minev B., Edman C., Deans R.J.;			
RT	"Identification of a novel melanoma gene (M650) - likely the gene for			
RT	IL-1 receptor antagonist - which encodes epitopes recognized by human			
RL	cytolytic T lymphocytes.";			
RL	Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; D86983; BAA13219.1; -.			
DR	EMBL; AF200348; AAF06354.1; -.			
DR	HSP; P05164; ICP.			
DR	GO; GO:0005152; F:Interleukin-1 receptor antagonist activity; NAS.			
DR	GO; GO:0006955; P:Immune response; NAS.			
DR	InterPro; IPRO02007; AnIm_peroxidase.			
DR	InterPro; IPRO07110; IG-like.			
DR	InterPro; IPRO03598; IG c2.			
DR	InterPro; IPRO01611; LRR.			
DR	InterPro; IPRO00483; LRR_Cterm.			
DR	InterPro; IPRO00372; LRR_Nterm.			
DR	InterPro; IPRO03591; LRR_Typ.			
DR	InterPro; IPRO02016; Peroxidase.			
DR	InterPro; IPRO01007; VWF C.			
DR	Pfam; PF03098; An_peroxidase; 1.			
DR	Pfam; PF00047; Ig_4.			
DR	Pfam; PF00560; LRR_5.			
DR	Pfam; PF01463; LRRCT; 1.			


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DR Pfam; PF00093; VWC; 1.
DR PRINTS; PRO0457; ANPEROXIDASE.
DR SMART; SM00408; IGC2; 4.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00013; LRNT; 1.
DR SMART; SM00369; LRR_TYP; 4.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50292; PEROXIDASE_3; 1.
DR PROSITE; PS01208; VWC_1; 1.
DR PROSITE; PS50184; VWC_2; 1.
DR Immunoglobulin domain.
FW NON_TER
SQ SEQUENCE 1496 AA; 167209 MW; E9B9A7069B1ABFF CRC64;

Query Match 10.0%; Score 131.5; DB 4; Length 1496;
Best Local Similarity 26.5%; Pred. No. 0.023;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9;

Oy 34 GDTVELTCTASQKKSIOFHMKNSNOIKILNGQSFLLTGPKSLNDRADRSRLMDQGNFP 93
Db 277 GNTVYFTCRAGNPPPEIIMLRNN-----NELSKTDSRLNLDLDDGT-- 318
Oy 94 LIINKLKIEDSDTYICEV-----EDQKEVDLVFGLTAN-----SDTHLLOGSILTL 141
Db 319 LMIQNTQRTDGIYQCMANKVAGEVKIQEVLTRYGFSPARPTFVIQPNTEVLVGESVTL 378
Oy 142 -----TLSEPPSSPSVQCRRSP---RCKNIQGGKTLVSQLELDSGTWTCTVLONOKV 193
Db 379 ECSATGHPPRPISWTRGDRPLPVDPRVNIPTSGGLYQIYNVQSGYACATNIDSV 438
Oy 194 EFKIDIVPRASALP---APFGSALPDQGT---ASALPDPPASAS 232
Db 439 HATAPII--VQALPQFTVTPDQRYVIEGQIVDFQCEAKGNPPVIA 482

RESULT 34
O8NPP4 PRELIMINARY; PRT; 955 AA.
AC O8NPP4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Glycoyl-phosphatidyl-inositol-MAM.
GN GPM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22077705; Pubmed=12082541;
RA De Juan C., Infesta P., Gonzalez-Quevedo R., Moran A.,
RA Sanchez-Pernate A., Torres A.J., Balbrea J.L., Diaz-Rubio E.,
RA Cruces J., Benito M.;
RT "Genomic organization of a novel glycosylphosphatidylinositol MAM gene
RT expressed in human tissues and tumors.";
RL Oncogene 21:3089-3094(2002).
CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL; AF478693; AA077220.1; -.
DR Genew; HGNC:19267; MDGA1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016163; F:nitrogenase activity; IEA.
DR GO; GO:0003399; P:nitrogen fixation; IEA.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000998; MAM_domain.
DR InterPro; IPR000318; Nitrogene_comp1.
DR Pfam; PF00047; IG; 6.
DR Pfam; PF00629; MAM; 1.
DR PRINTS; PRO0020; MAMDOMAIN.

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DR SMART; SM00409; IG; 6.
DR SMART; SM00408; IGC2; 6.
DR SMART; SM00137; MAM; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS50060; MAM_2; 1.
DR PROSITE; PS00699; NITROGENASE_1; 1.
DR Glycoprotein; Immunoglobulin domain.
FW NON_TER
SQ SEQUENCE 955 AA; 105790 MW; BD41A1EB10A05962 CRC64;

Query Match 9.9%; Score 130; DB 4; Length 955;
Best Local Similarity 23.2%; Pred. No. 0.0044;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

Oy 36 TVELTCTASQKKSIOFHMKNSNOIKILNGQSFLLTGPKSLNDRADRSRLMDQGNFP 95
Db 152 TVFLRCTVNSNPPPRFTWKRSD-----TLHSQDNG-VDIYEPLYTGERTKVL 199
Oy 96 -IKNLKIEDSDTYICEVEDQKE---EVQLVFGITANSPTHLLOGSILTLSEPPSSP 151
Db 200 KLKMLRQDYASVTCQSVANVCGIPDKATIFRLTNTTAPALK-LVNETLVNPGENV 258
Oy 152 SVQC-----RSPRKNIQGGKTLVSQLELDSGTWTCTVLON 189
Db 259 TVQCLITGSDPLPOLQWSHGPGPLALGALAQGG-TLSIPSVQARDSGYNTCTATNN 313

RESULT 35
O8IV49 PRELIMINARY; PRT; 338 AA.
AC O8IV49;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to limbic system-associated membrane protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Colon;
RA Straube R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033803; AA033803.1; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 338 AA; 37393 MW; 88CF00E07302817B CRC64;

Query Match 9.9%; Score 130; DB 4; Length 338;
Best Local Similarity 23.2%; Pred. No. 0.0044;
Matches 57; Conservative 40; Mismatches 91; Indels 58; Gaps 11;

Oy 10 LLLVQLALLPAA-----TQGNKVLGKGDVVELTCTASQKKSIOFHMKNSNOIKI 61
Db 14 LVLLRLCLLPPTGAPVSVDFNRTGNTIYRQSGTALIRCVEDKNS-KVAMLRSGIIF 72
Oy 62 LKNGSFLTGPKSLNDR--DSRRSLMDQGNFPILIKNLKIEDSDTYICEVEDQKE--- 116
Db 73 AGHD-----KMSLDRAVELEKRHSI---EYSLRIQKVDVDEGSYTSVQTHPEPT 121
Oy 117 -EVQLVFG---LTANSPTHLLOGSILTLSEPPSSPSVQCRR--SPRKNIQGGKT- 168
Db 122 SQVTLIVQVPPKSNISSDVTANEGSVTLVCMANGRPPEVITWRHLTPGREGESEY 181
Oy 169 LSVSQLELDSGTWTCTVLQ-----NOKVVEFKIDIVP-----RA 203
Db 182 LEIIGITREOSGKVECAANEVSSADVQKVTNVPPTITSEKSNATTTGRQSLKCEA 241

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QY 204 SALPAP 209
DB 242 SAVPAP 247

RESULT 36

Q90Y38 PRELIMINARY; PRT; 1259 AA.

AC Q90Y38; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Neural cell adhesion molecule L1.
GN L1CAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RE SEQUENCE FROM N.A.
RA Platzner M., Brenner V., Reichwald K., Wiene T., Oksche A.,
RA Rosenthal A.;
RT "Comparative sequence analysis of the mouse L1cam locus and the
RT corresponding region of human Xq28.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133093; AAF22153.1; -.
DR HSP; P20241; ICFB.
DR MGD; MGI:96721; L1cam.
DR GO; GO:0007411; P:axon guidance; IMP.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 6.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PSS0835; IG_LIKE; 6.
KM Immunoglobulin domain.
SQ SEQUENCE 1259 AA; 140916 MW; 25743C039892A22F CRC64;

Query Match 9.8%; Score 130; DB 11; Length 1259;
Best Local Similarity 23.9%; Pred. No. 0.005;
Matches 56; Conservative 32; Mismatches 96; Indels 50; Gaps 9;

QY 10 LLLVQLALLPAAATQGNKVVIGKKGDVVELTCTASQKKSIO--FHWKNSQIKILGNQGS 67
DB 507 ILANLQVVEATQITQGPRAIEKKGAVTFCQASFPDSIQASITWMDGR----- 557
QY 68 FLTGPSPKINDRADRSRLMDQGNFPLIKLKIKIEDSDTYIC---EVEDQKEVOLVIF 123
DB 558 -----DLQGRGSDXYFIEDGR--LVIOSLDYSDGNSCVASTELDEVESPAQLLV 608
QY 124 GLTAN-----SDTHLQGSLLTLTLESPSPSVQCRSP-----RGKNIQGGKTL 169
DB 609 GSPEPVHLESDHILKQSGVHL--SW-----SPAEDHNSIEKYLIEFEDKEAPAKMF 662
QY 170 SVSOLQSDSGTWCTVVLQNKQVE--FKDIVRASALPAPPTGSAALPPQTA 221
DB 663 SLGKV-----PQNQSTLTSLKSPVHYTFRTVAINKYGPSPSVSETVVPEAA 712

RESULT 37

Q812P8 PRELIMINARY; PRT; 437 AA.

AC Q812P8; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Nectin-like protein 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RE SEQUENCE FROM N.A.
RA Gingrich J.R., D'Angelo A., Chang G.M., Greenberg N.M.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF538973; AANI6368.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PSS0835; IG_LIKE; 3.
SQ SEQUENCE 437 AA; 47593 MW; D23DB347F5E5F023 CRC64;

Query Match 9.8%; Score 129.5; DB 4; Length 437;
Best Local Similarity 19.8%; Pred. No. 0.0068;
Matches 57; Conservative 43; Mismatches 101; Indels 87; Gaps 12;

QY 10 LLLVQLALLPAAATQGNKVVIGKKGDVVELTCTASQKKSIOFHWKNS 57
DB 3 VFLCNLSLVPAASAKNKVKSGQGPELTQNTVVEGGTALITCRVDQNDNTSLQWSNPA 62
QY 58 QIKILGNQGSFLTGPSPKINDRADRSRLMDQGNFPLIKLKIKIEDSDTYICE---VEDQ 114
DB 63 Q-----QTLVFDKALADNRILVRA SMHE--LSISVDVSLSDGGYTCSLFTMPVK 114
QY 115 KEEVOLVIFGL-----TANS DTHLQGSLLTLTLESPSPSVQCR--SPRGKNIQGGKT 168
DB 115 TSKAVYLTIVGVEPEKPGISGSSPVMEGDLMOQLCKT--SGSKPAADIRFPKDKKIK---- 169
QY 169 LSVSOLQSDSGTWCTVVLQNKQVEFKID----- 198
DB 170 -DVKYLKKEDANKKRTV--SSTLDFRVDRSDDGVAIVICRVDSLSLNTPTPVAMQVLEI 225
QY 199 -IVPRASALPAP-----TGSALPDP-----QTASALPDP 227
DB 226 HYPRSVKIIIPSTFPQEGPLITCSKGRPLPEVPLWTKDGEPLDP 273

RESULT 38

Q8SP16 PRELIMINARY; PRT; 731 AA.

AC Q8SP16; 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Polymetric immunoglobulin receptor.
GN PIGR.

OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;

RE SEQUENCE FROM N.A.
RA Taylor C.L., Harrison G.A.;
RT "cDNA cloning of the polymetric immunoglobulin receptor of the
RT marsupial Macropus eugenii (tamar wallaby).";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF17205; AAK69593.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 5.
DR PROSITE; PSS0835; IG_LIKE; 3.
KM Receptor.
SQ SEQUENCE 731 AA; 80253 MW; 91BDF3BC347B8C17 CRC64;

Query Match 9.8%; Score 129; DB 6; Length 731;
Best Local Similarity 23.6%; Pred. No. 0.015;
Matches 65; Conservative 47; Mismatches 100; Indels 64; Gaps 11;

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QY  NRGVPRHLLVULQALLPRAQTGNKVULGGKGDYELCTASOK--KSIOPHMNSQI 59
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  SRGUSFDITQVGODSNLP---DSEVIITTEGKTVSINCPKEEVDQRKLCCKDDXS 175
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  KIL-----GNQGSFLTKGPEKLNDRADSRSLWDQGNPELIIKNLKIEDSDTYICEV-ED 113
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  CVLVIDSONNVGSDYT-----ERVFRISGTSKVFVVIISQFKRODVGTYICAVGED 222
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  QKEBVOLVULVGLTRANSDPHLL---QQQSILTL--TLESPPGSSPSVQCR----- 155
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  SAPRIQKTIVIKLLDPETELVYAEQGSATYLNCAIYSTAENPMYLCRIKADMTCDLVIN 283
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  -----SPRGKNI-----QGKTLVSQLELDSDGTMTCTYLNQOKUYE----- 194
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  SKGFTNNSTHGRIILFTPEBGSFSMITQYQKREDAELYHCGAENGEPSEKPIQALQLF 343
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY  -FKIDYPRASALPAPYTSALP-----DPQATASAL 224
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  VSEETVPKSPLVKVGSGGSVSVLTCHYPPKNNTL 379
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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ID	Q8BLK3	PRELIMINARY;	PRT;	341 AA.
AC	Q8BLK3;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Limbic system-associated membrane protein precursor.			
GN	BL30007004RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=C57BL/6J;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RT	the FANTOM Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK044845; BAC32117.1; "			
DR	MED; MGI:2442078; BL30007004RIK.			
DR	InterPro; IPR003599; IG_1like.			
DR	InterPro; IPR007110; IG_1like.			
DR	InterPro; IPR003598; IG_c2.			
DR	Pfam; PF00047; IG_3.			
DR	SMART; SM00409; IG_3.			
DR	SMART; SM00408; IGC2; 3.			
DR	PROSITE; PS50835; IG LIKE; 3.			
SO	SEQUENCE 341 AA; 38086 MW; 949CE792C67E25C3 CRC64;			
Query Match		9.6%; Score 126; DB 11; Length 341;		
Best Local Similarity		22.8%; Pred. NO.0.0099;		
Matches	56; Conservative 41; Mismatches 91; Indels 59; Gaps 11.			
OY	10 LLLVQLALLPA-----TQGNKVVLGKKGDVVELCTASQSKSIQTHKNSNQIKI 61			
DB	14 LVLLRLCLLEPTGPEVRSVDFNRGDNITVROGDPAIRCVAVEDKNS-KVAMLNRSGLIF 72			
OY	62 LGNGGSFLTKGPSKLNDR--DSRRSLMDQGNFPLIKNLKIEDSDYICEVEDQK----- 116			
DB	73 AGHD-----KMSIDPRVELEKRAL-----EYSLRIQKVDYIDEGSTCSVQTHPEKT 121			
OY	117 -EVOLLVFG-----LTANSDFHLQGSILTLLESPGSSPSVOCR--SPRGKNIQSGKT- 168			
DB	122 SQVLLIVGVPRKISISSDVTWVESANTLVICMANGREPIVYTWHLPLRGREFGEDEY 181			
OY	169 LSVGLEIQDSGTWTCTVQLQ-----NQKKVEFKDIVP-----RA 203			

Dd	182	LEILIGTTREDSOGKYECKANEVSADVQKVQKTVVNPPTTIESKSNETHGROASLCEA	241
Qy	204	SALPAP	209
		:	
Dd	242	SAVPAP	247

RESULT	40			
ID	Q13857	PRELIMINARY;	PRT;	226 AA.
AC	Q13857;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Biliary glycoprotein (Fragment).			
GN	BGP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89139550; PubMed=2537311;			
RA	Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,			
RA	Elting J.J., Kanarck M.E.;			
RT	"Carchoembryonic antigen gene: alternative splicing accounts for the			
RT	multiple mRNAs that code for novel members of the carcinoembryonic			
RT	antigen family.";			
RL	J. Cell Biol. 108:267-276(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91140765; PubMed=8423792;			
RA	Barnett T.R., Drake L., Pickle W. II.;			
RT	"Human biliary glycoprotein gene: characterization of a family of			
RT	novel alternatively spliced RNAs and their expressed proteins.";			
RL	Mol. Cell. Biol. 13:1273-1282(1993).			
EMBL	M76741; AA57141.1; "			
GO	GO:0005624; C:membrane fraction; TAS.			
GO	GO:0007565; P:pregnancy; TAS.			
InterPro	IPR007110; IG-like.			
InterPro	IPR003598; IG_c2.			
Pfam	PF00047; IG_1.			
SMART	SM00408; IGC2; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin domain.			
NON_TER	1			
SEQUENCE	226 AA; 24045 MW; BE11929059866970 CRC64;			

	Query Match	9.5% ; Score 125.5 ; DB 4 ; Length 226 ;
	Best Local Similarity	24.7% ; Pred. No. 0.0064 ;
	Matches	63 ; Conservative 37 ; Mismatches 86 ; Indels 69 ; Gaps 13 ;
Oy	11 LVLQALLPAAQ--GNKRVLGKKGDVTELTCTASQKK-SIOFHWKNNSOIKILNQG	66
Db	24 IIVLLESPVVAKPPIKASKTTVTGDK-DSVALTSTSDTGISIMVFNNOST-----	74
Oy	67 SFLTKGSKLNDRAISRSLMDQNFPLINKLIKIEDSYTICEV-----EDQKEEVL-	120
Db	75 -----PS-----SERMKLSQGNTLLSINPVAREAGATCEVPFNISNGQDPMLN	121
Oy	121 -LVFGLTANSDTHLLQSQSLTLTESPPGSSPSVQCSPRCKNIQGGKTLSVSQLELODS	179
Db	122 EMAF-----HRTVARAGKLTSSNMPASTSGAATITERQN-----TWLPRLDS	165
Oy	180 GTWTCITVLQONQKVEFKIDIVPRASALPAPPTSGALPDPCITASLPDPAPASALPALAY	239
Db	166 NSMAQAQL-----PSVSO-QSAETTDNALQENGELS-----PGAIAGI--VIGV	205
Oy	240 ISFLSLGLGVACVL	254
Db	206 VALVALIAVALACFL	220

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RESULT 41
Q80U60 PRELIMINARY; PRT; 1431 AA.
ID Q80U60;
AC Q80U60;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MKIAA0230 protein (Fragment).
GN MKIAA0230.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10099;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22579291; PubMed=2693553;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
RA Nakajima D., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT II. The complete nucleotide sequences of 400 mouse KIAA-homologous
RT cDNAs identified by screening of terminal sequences of cDNA clones
RT randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:35-48(2003).
DR EMBL: AK122223; BAC65505.1;
DR GO: GO:0004601; F:peroxidase activity; IEA.
DR GO: GO:0006979; P:response to oxidative stress; IEA.
DR InterPro: IPR002007; AnIm_peroxidase.
DR InterPro: IPR003599; IG_1-like.
DR InterPro: IPR007110; IG_2-like.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003596; IG_V.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR004083; LRR_Cterm.
DR InterPro: IPR007092; LRR_SDS22.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR002016; Peroxidase.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF03098; An_peroxidase; 1.
DR Pfam: PF00047; IG_4.
DR Pfam: PF00560; LRR; 5.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF00093; VWC; 1.
DR PRINTS: PRO0457; ANPEROXIDASE.
DR SMART: SM00409; IG; 4.
DR SMART: SM00408; IGc2; 4.
DR SMART: SM00406; IG; 3.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00366; LRR_PS; 4.
DR SMART: SM00369; LRR_Typ; 5.
DR SMART: SM00214; VWC; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS50292; PEROXIDASE_3; 1.
DR PROSITE: PS01208; VWF_C_1; 1.
DR PROSITE: PS50184; VWF_C_2; 1.
FT NON TER 1
SQ SEQUENCE 1431 AA; 160591 MW; 6BA952436DA54B72 CRC64;

Query Match 9.5%; Score 125.5; DB 11; Length 1431;
Best Local Similarity 25.0%; Pred. No. 0.072;
Matches 57; Conservative 25; Mismatches 93; Indels 53; Gaps 9;

QY 34 GDTVELICTASQKSIQFHWKNSNQITLNGQSFLLTKGSKLNDKDRSLMDQGNFP 93
DB 213 GNTVYFTCRAGNKPRIIMLRNN-----NELSMKTSRLNLDGCT-- 254
QY 94 LIINKLIEDSDTYICEV-----EDQKEVQLLVFGLTAN-----SDPHLQGGSLTL 141
DB 255 LMIQNTCEABEGVYQCAKNAVGAKEAQVETLRLTSSPARPTFYIQNTVEVLGSS--V 312
QY 142 TLSPSPSSPSPVQCRSPRGK-----NIQGGKTLVSQLELQDSGTWCTVLQNOK 191
DB 313 TLSCSAGHPLPQTLTWTRGRDTPPLPIDPRVITPSSGLYIQNVANQSDSGEYTCASNSVD 372
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QY 192 KVEFKIDIVPRASALP---APPTGSALPDPQT-----ASALPDPRAA 230
DB 373 SIHATAFI--VQALPQFTVTPQSRVIEGQVTDQCAKGHQPPIA 418

RESULT 42
Q87A95 PRELIMINARY; PRT; 332 AA.
ID Q87A95;
AC Q87A95;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to CMRF3 antigen precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RX Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC025395; AAH25395.1;
DR InterPro: IPR003599; IG_1-like.
DR InterPro: IPR007110; IG_2-like.
DR Pfam: PF00047; IG_1.
DR SMART: SM00409; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
SQ SEQUENCE 332 AA; 36059 MW; 159124621383CE93 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.012;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLQALPLA--ATQGNKVLGKKDYTELTCTASQK--KSIQFHWKNSNQIKLGN 64
DB 2 RLVLVLMGCLLPYGALEGPBEISGFBEDTVSLQCTYBELRDHKVCKRKGILFNSC 61
QY 65 QGSFLT--KQPSKLNRA--DSRSLMDQGNPPLIINKLKIEDSDTYICEVDQKEVYA 119
DB 62 SGTYAEEGQETMKRVSIRDSRQEL---SLIVTLMNLTLDAGEVCGVEKRPDES 117
QY 120 LVVFGLTANSDPHLQGGSLTLTLESPPSSPSPVQCRSKRGNKIQGGKTLVSQLE---- 175
DB 118 LLI-----SLFVFPGPC-----CPSPSPPTFQ-----PLATRIQPKAK 151
QY 176 -----LQDSGTWCTVLQNOKVEFKIDIVPRASAL-----PA--PPT 211
DB 152 AQQTQPPGLTSPFLYLAATTAQGTGAALPPLPGISQYGHERTSQYTGSRPHATSPRA 211
QY 212 GSALPDPQ--TASALPDPRAA-----LPAALAVISFLGLGLGVAC 252
DB 212 GSSRPMPQUNTSABEDTSPALSSGSKPRVSIPMVRI LAPVLVLSLSAAGLIAC 268

RESULT 43
Q80V81 PRELIMINARY; PRT; 358 AA.
ID Q80V81;
AC Q80V81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SC:d125023.3 (Novel immune-type receptor 1.10 (nltr1.10)).
GN SC:D125023.3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX Cyprinidae; Danio.
RN NCBI_TaxID=7955;
RP SEQUENCE FROM N.A.
RA Garner P.;
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RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL591405; CADI2581.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; 19.
DR InterPro; IPR007110; 19-like.
DR Pfam; PF00047; 19; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Receptor.
SQ SEQUENCE 358 AA; 40130 MW; BBAD75EBAEAB4953 CRC64;

Query Match 9.5%; Score 125; DB 13; Length 358;
Best Local Similarity 24.1%; Pred. No. 0.013;
Matches 59; Conservative 29; Mismatches 85; Indels 72; Gaps 10;

QY 24 QGNKVLGKGDYELTCTASQKSIQPHM---KNSNQIKLNGQSFLTGP----- 73
DB 56 QENNVIQAGEVDNLCTFSPNMQLSTAFWKHTADGKTLQIVFN--LFTKSPIMNNV 113
QY 74 SKLNDRADSRSLMDQGNFPLIKLKIEDSDTYICEVEDK-----EEVQLVFGLTAN 128
DB 114 EKMD---VNVIIIEGFFNLTKTKPSDSATYCIYVSYQALGMGSGTRLIVDAATD 169
QY 129 SDTLLQGQSLTLTLESPGSSPSVQC-----NKKVEFKIDIVP 201
DB 170 RNTTL--HQSLIDTYD--FGDSVNLQCSIFTESCAGDHNIYFKQSSGSEGLYTKGR 225
QY 157 SPGRKNIQGGKT-----LSVSQLDELQSGTWCTVLIQ-----NKKVEFKIDIVP 201
DB 226 NGRCKNSAESETQSCVSLHKNNISRSPTYIYCAVACQILLNGTQLNIRSGDLYP 285
QY 202 RASAL 206
DB 286 ALLAL 290

RESULT 44
Q9H1X9 PRELIMINARY; PRT; 390 AA.
AC Q9H1X9;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE BG15303.1 (Similar to C.elegans hemicentin) (Fragment).
GN BG15303.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lawlor S.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL133515; CAC17584.1; -.
DR HSP; P56276; ITLK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; 19; 5.
DR SMART; SM00408; IGc2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KM Immunoglobulin domain
FT NON_TER 1
FT NON_TER 390
SQ SEQUENCE 390 AA; 42153 MW; E1F7B5D5BE6E19B4 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 390;
Best Local Similarity 23.3%; Pred. No. 0.014;
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

QY 34 GDTVELTCTASQKSIQPHMKNQIKLNGQSFLTGPCKLNDRADSRSLMDQGNF 93
DB 181 GSNVTLPCYVGPEPTIKMRLDNMPFSR--PFSVSSISQLRTGA----- 225

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QY 94 LIINKLIEDSDTYICEVEDK-----KEEVQLVFGLTAN-----NSDTHLQGSLTTL 143
DB 226 LFIINLWASDKGYTICAEENQFGKIQSETTYTGLVAPLIGISPSVANYIEGQTLPC 285
QY 144 ESPPGS-----SPSVQCRSPGRKNIQGGKTLVSQLELDQSGTWCTVL 187
DB 286 TLLAGNPIPERRWIKNSAMLLQNPYITVR-----DGLHIERVQLQGGGYTCVAS 337
QY 188 Q----NKKVEFKIDIVP---RASALPAPPGSALPPQTSALPDP 227
DB 305 NVAGTNKTKTSVVVHVLPTIQHGQQLISTIEGIPVTLPCRASGNPKP 384

RESULT 45
Q96DN8 PRELIMINARY; PRT; 512 AA.
AC Q96DN8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein FLJ31774.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hota T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamauchi H., Chiba Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishitawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK056336; BAB71154.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; 19; 6.
DR SMART; SM00408; IGc2; 5.
DR PROSITE; PS50835; IG_LIKE; 6.
KM Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 512 AA; 54971 MW; 9368150E8A5D6C8 CRC64;

Query Match 9.5%; Score 125; DB 4; Length 512;
Best Local Similarity 23.3%; Pred. No. 0.021;
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

QY 34 GDTVELTCTASQKSIQPHMKNQIKLNGQSFLTGPCKLNDRADSRSLMDQGNF 93
DB 148 GSNVTLPCYVGPEPTIKMRLDNMPFSR--PFSVSSISQLRTGA----- 192
QY 94 LIINKLIEDSDTYICEVEDK-----KEEVQLVFGLTAN-----NSDTHLQGSLTTL 143
DB 193 LFIINLWASDKGYTICAEENQFGKIQSETTYTGLVAPLIGISPSVANYIEGQTLPC 252
QY 144 ESPPGS-----SPSVQCRSPGRKNIQGGKTLVSQLELDQSGTWCTVL 187
DB 253 TLLAGNPIPERRWIKNSAMLLQNPYITVR-----DGLHIERVQLQGGGYTCVAS 304
QY 188 Q----NKKVEFKIDIVP---RASALPAPPGSALPPQTSALPDP 227
DB 305 NVAGTNKTKTSVVVHVLPTIQHGQQLISTIEGIPVTLPCRASGNPKP 351

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DT 01-OCT-2003 (TEMBLrel. 25, last annotation update)
 DE KLG protein (L010776P).
 GN KLG OR CG6669.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Aamane M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfennoch C., Baldwin D.,
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Buzam D.A., Butler H., Cadien E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Fodor B.C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ileguam C.,
 RA Ustall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinrock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RU [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkely;
 RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Fries E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Paclet J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AEO03741; AAF56071.1; -
 DR EMBL; AY060363; AAL25402.1; -
 DR FlyBase; FBgn0017590; klg.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig_3.
 DR SMART; SM00408; FN3; 1.
 DR SMART; SM00408; IGC2; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 545 AA; 60087 MW; DSE81D9E5574E9DB CRC64;

Query Match 9.5%; Score 125; DB 5; Length 545;
 Best Local Similarity 22.3%; Pred. No. 0.022;
 Matches 50; Conservative 36; Mismatches 100; Indels 38; Gaps 8;
 QY 2 NNGVPRHLLVLTAL-----LPAATQGNKVVLGKKGDTVELTCTASOKKSIOFHW 53
 DB 75 NNGSNRSMSNVQGSVAASLTATLPRFLSGHYRAVVGDTLVPCQVENLGNVLLM 134
 QY 54 KNSNQIKILGNQGSFLTKPPSKLNDRASSRLMDQGNFPLIIKLIKEDSDTICEV-- 111
 DB 135 RRGTVNLATASN--IWVTR-----DERVRLID--GYNLEISDLEPDADGYVCOISD 181
 QY 112 ---EDQKEVQL-----VFGLTANSPDTHLLQGSLLTLTESPPGSSPSVQCRSPRKN-- 162
 DB 182 KINRDVHTVELVLPSPVAIFPSGQLQARKGGPITLCKGSGNPVSIYWKSGANMS 241
 QY 163 ---IQGKTLVSQLELDQSGTWTCV---LQNKVKVEKIDIV 200
 DB 242 TARIGDPITLLEKLRQAGVYQCTADNGVDPTVDMRLDVL 285

RESULT 47
 ID 096RW7 PRELIMINARY; PRT; 5636 AA.
 AC 096RW7;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Hemolentin.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Trent J.;
 RT "Human hemolentin gene.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF156100; AA68690.1; -
 DR GO; GO:0005727; C:cytochromeosomal circular DNA; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR008875; Cecropin.
 DR InterPro; IPR001434; DUF11.
 DR InterPro; IPR001881; DUF11.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR009017; GFP_1like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR000169; SH3prot_acetate.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF00047; Ig; 44.
 DR Pfam; PF00090; tSP_1; 6.
 DR SMART; SM00179; EGF_CA; 7.
 DR SMART; SM00408; IGC2; 43.
 DR SMART; SM00209; TSP1; 6.
 DR SMART; SM00327; VWA; 1.
 DR TIGRFAMs; TIGR01451; B ant repeat; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 5.
 DR PROSITE; PS00268; CECROPIN; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 DR PROSITE; PS50835; IG_LIKE; 44.
 DR PROSITE; PS00639; TH1OL_PROTEASE_HIS; 1.
 DR PROSITE; PS50092; TSP1; 6.
 KW EGF-like domain; Immunoglobulin domain.
 SQ SEQUENCE 5636 AA; 613660 MW; F000B19CED7B52C CRC64;
 Query Match 9.5%; Score 125; DB 4; Length 5636;

Best Local Similarity 23.3%; Pred. No. 0.48;
Matches 53; Conservative 26; Mismatches 92; Indels 56; Gaps 8;

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OY 34 GDTVELTCTASQKSIQCHMKNSNOIKILGNGSFLTKGSPKLNDRADSRSLMDQGNF 93
DB 807 GSNVTLPCYVOGYEPPTIKMRLLDMPFISR--PFSVSSISQLRGA----- 851
OY 94 LIKKLKIEDSDTYICEVEDQ-----KEEVQLLVFGLTA-----NSDTHLLOGSLTLTL 143
DB 852 LFIPLNLMASDKCTYICEANOGCKIQSETTYVTTLVLPFGISPSVANVIEGQQLLPC 911
OY 144 ESPSGS-----SPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWCTVL 187
DB 912 TLGNPNPIPERKWKNSAMLLQNPITYRS-----DGLHIERVQLDQGGERTCVAS 963
OY 188 Q----NOKKVEFKIDIVP---RASALPAPPTGSALPDPTQTSALPDP 227
DB 964 NVAGTNNKTSVVAHLEPTIOHQOILSTIEGIPVTLPCCKASGNPKP 1010

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RESULT 48

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OY Q9EOK9 PRELIMINARY; PRT; 394 AA.
AC Q9EOK9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE NK cell receptor 2B4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=PVG;
RX MEDLINE=21173196; PubMed=11275258;
RA Kumarasan P.R., Stepp S.E., Verreut P.C., Chuang S.S., Boles K.S.,
RA Lai W.C., Ryan J.C., Bennett M., Kumar V., Mathew P.A.;
RT "Molecular characterization of the rat NK cell receptor 2B4.";
RL Mol. Immunol. 37:735-744(2000).
DR EMBL; AF209406; AAC35766.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
KW Receptor.
SQ SEQUENCE 394 AA; 44286 MW; 6F917EF02C542198 CRC64;

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Query Match 9.5%; Score 124.5; DB 11; Length 394;
Best Local Similarity 21.1%; Pred. No. 0.016; Matches 92; Indels 115; Gaps 12;
Matches 64; Conservative 33; Mismatches 92; Indels 115; Gaps 12;

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OY 12 LVQLALPAAATG-----NKVVLGKKGDTVELTCTASQKSIQCHMKNSNOIKILGNQ 65
DB 6 VLSLFLRLRAHQGDGASGSEVLGVGSKPRLRPSNIQTKHSIEK----- 54
OY 66 GSFLTKGSKLNDRADSRSLW-----DQGNFLLIKLKIEDSDTY 107
DB 55 -----KKTGHQQTSHIVMTLDPESPVCSDIYGFESENFALSIKAKINDSGHY 106
OY 108 ICEVEDQ-----KEEVQLLVF-----GLTANSQTHLLOGSLTLTLSPSGSS 150
DB 107 LLEIITDQGGIVCTKPFQILFDPVETPHLTVQGSILMANGTQL----- 149
OY 151 PSVQCRSPRGKNI-----QGGKTLVSQ-----LELDQSGTWCTVLNOKKVEFKI 197
DB 150 -SLSCFVXKDNVSAVALRGSMLISNQRNGHWMEMTASSLHTYTGVNSK----- 200
OY 198 DIVPRASALPAPPTGSALPDPTQTSALPDPAASALPALAV---ISFLILGLGVACVL 254
DB 201 -----ASMANHTLSPQSCQSVPS--KFNVLPPVVISGILVTFLLG-ALACFCW 247
OY 255 ARTR 258

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DB 248 NRKR 251

RESULT 49

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OY Q98923 PRELIMINARY; PRT; 504 AA.
AC Q98923;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HEMCAM precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=H.B190v+; TISSUE=Thymus;
RX MEDLINE=97133433; PubMed=8978830;
RA Valin O., Dunon D., Alsel F., Dangy J.P., McNaghy K.M., Imhof B.A.;
RT "HEMCAm, an adhesion molecule expressed by c-Kit+ progenitors.";
RL J. Cell Biol. 135:1655-1668(1996).
DR EMBL; Y08854; CAAT0079.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 35
FT CHAIN 36 504
FT SEQUENCE 504 AA; 55540 MW; ADAE4B94ED4F02E1 CRC64;

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Query Match 9.5%; Score 124.5; DB 13; Length 504;
Best Local Similarity 23.7%; Pred. No. 0.022; Matches 88; Indels 43; Gaps 6;
Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

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OY 19 LPAATQGNKVVVLGKKGDTVELTCTASQKSIQCHMKNSNOIKILGNGSFLTKGSPKLN 78
DB 268 LRVATNAGIV---KEGDDVKLVCDAD-----GNAPAVPSFRRRLGD 306
OY 79 RADSRSLMDQGNFLLIKLKIEDSDTYICEVED-----QKEVQLLV-----FGL 125
DB 307 SWQDMTSLADTNDGVLMHLNHSKSSGGLYRCQTLDDMTQHEGDELVNVVYIEGVQVKM 366
OY 126 TANSQTHLLOGSLTLTLSPSGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWCT 185
DB 367 EPSSPLH--EGDSVRLCTAHSPVKLDYQWRDARGRYAEGNQLLTNLTFTETSSNFSR 424
OY 186 V-----LONOKKVEFKIDIVPRASALPAP 209
DB 425 VKARSVPGLGSKQVAVAVKGRIVVAISAP 455

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RESULT 50

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OY Q98921 PRELIMINARY; PRT; 584 AA.
AC Q98921;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE HEMCAM precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=H.B190v+; TISSUE=Thymus;
RX MEDLINE=97133433; PubMed=8978830;

```

RA Vainio O., Dunon D., Aissi F., Dangy J.P., McNagny K.M., Imhof B.A.;
RT "HEMCM" an adhesion molecule expressed by c-kit+ progenitors.";
DR EMBL: Y08856; CAA70081.1; -
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG; 5.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PSS0835; IG-LIKE; 5.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 584 POTENTIAL.
SO SEQUENCE 584 AA; 64422 MW; 5972D946604AF6F3 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 584;
Best Local Similarity 23.7%; Pred. No. 0.027;
Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGSFLTKGSPKLAND 78
Db LRAVATNAGIV---KEGDVAVLCDDA-----GNPAVPSFPRRELGD 306

QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125
Db SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366

QY 126 TANSPTHLQGSILTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185
Db EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSNFSR 424

QY 186 V-----LONOKVEFKIDIVPRASALPAP 209
Db VKARSVGLEQSKQVAVAVGKPRIVAIISAP 455

RESULT 51
Q09089 PRELIMINARY; PRT; 584 AA.

AC Q09089;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE S-gicerin.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn; TISSUE=Gizzard;
RX MEDLINE=94213753; PubMed=8161437;
RA Taira E., Tachihara N., Taniura H., Kim C., Miki N.;
RT "Molecular cloning and functional expression of gicerin, a novel cell
adhesion molecule that binds to neurite outgrowth factor.";
RT Neuron 12:861-872(1994).
RL
RN
RT
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Leghorn; TISSUE=Gizzard;
RX MEDLINE=96081930; PubMed=7499388;
RA Taira E., Negino T., Taniura H., Takaha N., Kim C., Kuo C., Li B.,
Higuchi H., Miki N.;
RT "Expression and functional analysis of a novel isoform of gicerin, an
immunoglobulin superfamily cell adhesion molecule.";
RT J. Biol. Chem. 270:28681-28687(1995).
RL
DR EMBL: D36559; BAA07563.1; -
DR PIR: I50419; I50419.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PSS0835; IG-LIKE; 4.
KW Immunoglobulin domain.

SO SEQUENCE 584 AA; 64378 MW; 876E0C3E920BA92F CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 584;
Best Local Similarity 23.7%; Pred. No. 0.027;
Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGSFLTKGSPKLAND 78
Db LRAVATNAGIV---KEGDVAVLCDDA-----GNPAVPSFPRRELGD 306

QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125
Db SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366

QY 126 TANSPTHLQGSILTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185
Db EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSNFSR 424

QY 186 V-----LONOKVEFKIDIVPRASALPAP 209
Db VKARSVGLEQSKQVAVAVGKPRIVAIISAP 455

RESULT 52
Q09092 PRELIMINARY; PRT; 626 AA.

AC Q09092;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HEMCAM precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H-B190v+; TISSUE=Thymus;
RX MEDLINE=97133433; PubMed=8978830;
RA Vainio O., Dunon D., Aissi F., Dangy J.P., McNagny K.M., Imhof B.A.;
RT "HEMCM, an adhesion molecule expressed by c-kit+ progenitors.";
RT J. Cell Biol. 135:1655-1668(1996).
RL EMBL: Y08855; CAA70080.1; -
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG; 5.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PSS0835; IG-LIKE; 5.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 626 POTENTIAL.
SO SEQUENCE 626 AA; 69104 MW; 27F8F2F47044E163 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 626;
Best Local Similarity 23.7%; Pred. No. 0.03;
Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

19 LPAATQGNKRVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNGSFLTKGSPKLAND 78
Db LRAVATNAGIV---KEGDVAVLCDDA-----GNPAVPSFPRRELGD 306

QY 79 RADSRRLMDQGNFPLIINKLIKEDSDTYICEVED-----OKEEVQLLV-----FGL 125
Db SWQDMTSLADTNDGVLMHNVSXSSGLYRCQTLDDMTQHEGDVELVNNYIEGVQVKM 366

QY 126 TANSPTHLQGSILTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSGTWCT 185
Db EPSSPLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTNLTFETSNFSR 424

QY 186 V-----LONOKVEFKIDIVPRASALPAP 209
Db VKARSVGLEQSKQVAVAVGKPRIVAIISAP 455

RESULT-53

Q90880 PRELIMINARY; PRT; 626 AA.
 AC Q90880;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE L-glicerol.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lehman; TISSUE=Gizzard;
 RX MEDLINE=6081930; PubMed=749938;
 RA Taira E., Nagino T., Taniguchi H., Takaha N., Kim C., Kuo C., Li B.,
 RA Higuchi H., Miki N.,
 RT "Expression and functional analysis of a novel isoform of glicerol, an
 immunoglobulin superfamily cell adhesion molecule."
 RL J. Biol. Chem. 270:28681-28687 (1995).
 DR EMBL; D49849; BAA08648.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00408; IGc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 KM Immunoglobulin domain.
 SQ SEQUENCE 626 AA; 69074 MW; C4791BECCE55133 CRC64;

Query Match 9.5%; Score 124.5; DB 13; Length 626;
 Best Local Similarity 23.7%; Pred. No. 0.03;
 Matches 50; Conservative 30; Mismatches 88; Indels 43; Gaps 6;

QY 19 LPATQGNKVVLGKKGDVLTCTASQKSIQFHMKNNOIKLGNQSGFLTKGPSKLAND 78
 DB LRVATNAGIV--KEGDVVKLVCDAD-----GNPAPVPSFRRRLGD 306
 QY 79 RADRSRLMDQGNFPLIKIKIEDPTVCEVED-----QKEEVOLLV-----FGL 125
 DB 307 SMQMTSLADPNDGVLMHNVSKSSSGLYRCQTDLDMDTHQEGDVELVAVYVIGVQVM 366
 QY 126 TANSDFHLLQGSLLTLTSSPGSSPSVQCRSPGKNIQGGKTLISVQLQDSGTWCT 185
 DB 367 EPPSPFLH--EGDSVRLSCTAHSPVKLDYQWRDARGKVAEGNQLLTTLVTFRTSSNFSR 424
 QY 186 V-----LONQKVEPKIDIVPRASALPAP 209
 DB 425 VKARSVPGLEQSKQVAVAKGPRIVASIP 455

RESULT 54

Q9NR99 PRELIMINARY; PRT; 2828 AA.
 AC Q9NR99;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Adlican.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Crowl R.M., Luk D.,
 RT "Identification of the gene encoding Adlican, a novel protein
 expressed in human arthritic tissues."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF245505; AAF86402.1; -
 DR HSSP; P56276; ITLK.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_cyp.
 DR Pfam; PF00047; Ig; 12.
 DR Pfam; PF00560; LRR; 6.
 DR Pfam; PF01463; LRRCT; 1.
 DR SMART; SM00408; IGc2; 10.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00013; LRNT; 1.
 DR SMART; SM00369; LRR_TYR; 3.
 DR PROSITE; PS50835; IG_LIKE; 12.
 KM Immunoglobulin domain.
 SQ SEQUENCE 2828 AA; 312291 MW; A18377D8554F1FE1 CRC64;

Query Match 9.5%; Score 124.5; DB 4; Length 2828;
 Best Local Similarity 23.1%; Pred. No. 0.21;
 Matches 56; Conservative 36; Mismatches 83; Indels 67; Gaps 12;

QY 22 ATQGNKVVLGKKGDVLTCTASQKSIQFHMKNNOIKLGNQSGFLTKGPSKLAND 81
 DB 484 AVGRDQTVL--EGGPQLSCNVKASBPSTFW-----VLPD-GSIL-KAPM---DDPD 529
 QY 82 SRSLMDQGNFPLIKIKIEDPTVCEVEDQKEEVOLLVFGITANSDFHLLQGSFLT 141
 DB 530 SKFSILSSG--WLRIKMEPSDSGLYOC-IAQVDEMDRMVRYLVQSPS--TQPAERDV 585
 QY 142 TLSPSPSSPSVQCRS-----PRKNIQGGKTLV 171
 DB 586 TIGKNPESVTLPCNALAIPAHLSWILPNRIINDIANTSHVYMLNG-----TLST 638
 QY 172 SOLELOSGTWTCTVLOQKVEFKIDIVPRASALPAPGSAIPDPQASALPDPAPAS 231
 DB 639 PKVQVSSSGYRCVAVVQAGADHTVGIT-----VTKGGSLPSRGRR-----FGAK 686
 QY 232 AL 233
 DB 687 AL 688

RESULT 55

Q8UV52 PRELIMINARY; PRT; 325 AA.
 AC Q8UV52;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE SC:d2263j20.6 (Novel immune-type receptor).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hammond S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL591476; CAD21600.1; -
 DR GO; GO:0004872; F:receptor activity; IBA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KM Receptor.
 SQ SEQUENCE 325 AA; 36190 MW; 01F5BCE2055EE064 CRC64;

Query Match 9.4%; Score 124; DB 13; Length 325;

Best Local Similarity 23.7%; Pred. No. 0.014;
Matches 57; Conservative 33; Mismatches 88; Indels 64; Gaps 9;
QY 24 QGNKRVVLGKKKGVDELVTCTASOKKSIQFHN-----KSNNOIKILGNQSGFLTKGSPSKLN-- 77
DB 23 QENNVKIVGQGEEDVNLCTFSPNMQLSTAMFKHTADOKTLQIVFN--LFFTKSPIMNNV 80
QY 78 DRADRSRLMDQGNFPLIKNLKIEDSDTYICEVEQK-----EYQVLVFGILANSDPH 132
DB 81 EKNNNVNVIIEEGFNLTKTKPSDAIYCVVSSYQALGMGSGTLLIVRADATDRNTT 140
QY 133 ILQGOSLTLTSSPGSSPSVQC-----RSPRG 160
DB 141 L--HQSLIDTVD--PGDSVNLQCSIFTESCAGDSHYWFKQSGDSEGVLYTKGEANGRC 196
QY 161 KNTQGCKT-----LSVSQLELDGSGTCTVTLQ-----NKKVEFKDIVPRASA 205
DB 197 KNSAESPTQSCVSVLHKNNISRSDDTYIYCAVAACQILGNQTQINIRESGDLYPALTA 256
QY 206 L 206
DB 257 L 257
RESULT 56
ID 063669 PRELIMINARY; PRT; 739 AA.
AC 063669;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Vascular cell adhesion molecule 1 precursor.
GN VCAM-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague Dawley; TISSUE=Lung;
RX MEDLINE=92305064; PubMed=137031;
RA Williams A.J., Atkins R.C., Fries J.W., Gimbrome M.A.Jr.,
RA Cybulsky M.J., Collins T.;
RT "Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.";
RL Biochim. Biophys. Acta 1131:214-216(1992).
DR EMBL; X63722; CAA45254.1; -;
DR HSSP; P19320; IVCA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016337; P:cell-cell adhesion; IEA.
DR InterPro; IPR003987; ICAM VCAM-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003989; VCAM-1.
DR Pfam; PF00047; Ig_5.
DR PRINTS; PR01472; ICAMVCAM1.
DR PRINTS; PR01474; VCAM1.
DR SMART; SM00408; ICG2; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 24
FT CHAIN 25 739 VASCULAR CELL ADHESION MOLECULE 1.
SQ SEQUENCE 739 AA; 81136 MW; ASAAD1172F67F9B6 CRC64; #
Query Match 9.4%; Score 124; DB 11; Length 739;
Best Local Similarity 23.4%; Pred. No. 0.041;
Matches 43; Conservative 30; Mismatches 71; Indels 40; Gaps 5;
QY 33 KGVDELVTCTASOKKSIQFHNKNNQIKILGNQSGFLTKGSPSKLNDADRSRLMDQGNF 92
DB 238 EGAANVTTCASGEGPAPETFSK-----LDNGVQLL-----SGNA 274
QY 93 PLIKNLKIEDSDTYICEVEQK-----VEDQKEVQLLV-----FGLTANSDDLQSGSLTLT 142

DB 275 TLTLIAMRMEDSGIYVCEGNVLGRDKTEVELLVOEKPTVDISPSQVAAGVDSVLT 334
QY 143 LESPPGSSPSVQCRPRGNKINQ-----GTLISVSQLELDGSGTCTVTLQNKVKRF 195
DB 335 CAAVGDSPSFSFMRQTDSPLNGEVRDEGATSTLTLSPGVDEHSHLYLCTVCRKLEK 394
QY 196 KIDI 199
DB 395 TIQV 398
RESULT 57
ID 09VLF0 PRELIMINARY; PRT; 532 AA.
AC 09VLF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG31708-PA (CG31708-PB).
GN CG31708.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jajal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tjdy J.L., Bergman C.M., Bertman B.P., Carlson J.W., Celniker S.E.,
RA Clamp M.E., Drysdale R.A., Emmert D., Fries E., de Grey A.D.N.J.,
RA Harris N.L., Krommiller B., Millburn G.H., Richter J.,

RA Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,
 RA Whitefield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
 RA Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome."
 RN Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RL (3)
 RA FLYBASE;
 RP SEQUENCE FROM N.A.
 RN Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 RL (4)
 RP SEQUENCE FROM N.A.
 RA FLYBASE;
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AE003623; AAF52743.3; -
 DR FLYBASE: FBgn0051708; CG31708.
 DR InterPro: IPR003599; IG_1.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; IG_2.
 DR SMART: SM00409; IG_3.
 DR SMART: SM00408; IGC2; 3.
 DR PROSITE: PS50835; IG_LIKE; 3.
 SQ SEQUENCE 532 AA; 56872 MW; 67D3D39A270FE22E CRC64;
 Query Match 9.3%; Score 122.5; DB 5; Length 532;
 Best Local Similarity 20.8%; Pred. No. 0.036; Indels 41; Gaps 7;
 Matches 47; Conservative 41; Mismatches 97;
 QY 5 VPFRLHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIKILGN 64
 DB 101 VPTNSLNINIVE---EPEFTYIENVTVAGRNIVKLGSGVKMIGSKVAMHFEQSALITV 157
 QY 65 QGSFLTKGP--SKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQLLV 122
 DB 158 HNHVITRNPRISVTHDKIDRHRWTY-----LHINNVEIEDRGRMCQINTVTAKTQ--- 208
 QY 123 FGL-----TANSDPHLLQGOSLTLTLESPPSSPSVOCSPRGKNIQ----- 164
 DB 209 FGYNLVVVPINIDSLSSDVIYREGANISLRCASSPRLIIKKRDNRIAMINKHI 268
 QY 165 ---GKTLVSQLELDQSGTWTCTVLON-----QKKEVFKIDIVP 201
 DB 269 VNEWEGDTLEITRISRLMGAVLCTASNGVPTVSKRIKVSVDPPP 314
 RESULT 58
 ID Q723B1 PRELIMINARY; PRT; 355 AA.
 AC Q723B1;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein DKFZP686B1946 (Fragment).
 GN DKFZP686B1946.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human amygdala;
 RA Amosgo W., Krieger S., Regiert T., Rittmuller C., Schweiger B.,
 RA Meyer H.W., Weil B., Andl C., Osanger A., Fobo G., Han W., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BX538014; CAD97961.1; -
 DR Hypothetical protein.
 KW NON TER
 FT 1
 SQ SEQUENCE 355 AA; 38776 MW; 67CA457F160FAD15 CRC64;
 Query Match 9.3%; Score 122; DB 4; Length 355;
 Best Local Similarity 23.0%; Pred. No. 0.023;
 Matches 53; Conservative 36; Mismatches 93; Indels 48; Gaps 10;

QY 20 PAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIKILGNQSGFLTKGP-----SK 75
 DB 42 PMAVDMMV--RKGDTAVLRCTYEDGAS--KGALNNSSTIFAG--GDKMSVDRVSI 96
 QY 76 LNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVLVFGILT----- 127
 DB 97 LNKR-----DYSLQIENVDTVDGDTCSQVQHTPRITMQVH--LTVQVPPKIYD 144
 QY 128 -NSDTHLLQGOSLTLTLESPPSSPSVQCR--SPRGNIQGKTLVSQLELDQSGTWTCT 184
 DB 145 ISNDTVNEGTVTLTCLATGKPPPSISWRHISPAKPFENGQYLDITGTRDQAGEYEC 204
 QY 185 TV-----LQNKKEFKIDIVPRASALPAPT-----GSALPDP 218
 DB 205 SAENDVSPDVRAKVVVNFAPTIQELKSGVTPTGRSGLRCEAGVPPP 254
 RESULT 59
 ID O93250 PRELIMINARY; PRT; 1009 AA.
 AC O93250;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Contactin A.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J; TISSUE=Brain;
 RA Nagata S., Suzuki A.;
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J; TISSUE=Brain;
 RA Nagata S., Fujita N., Takeuchi K., Watanabe K.;
 RT "cDNA cloning and expression of the Xenopus homologue of the neural
 cell adhesion molecule, contactin (F3/Fl1).";
 RL Zool. Sci. 13:813-820 (1997).
 DR EMBL: AB015205; BAA28780.1; -
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00047; FN3; 4.
 DR Pfam: PF00047; IG; 6.
 DR SMART: SM00060; FN3; 4.
 DR SMART: SM00408; IGC2; 3.
 DR PROSITE: PS50835; IG_LIKE; 6.
 KW Immunoglobulin domain.
 SQ SEQUENCE 1009 AA; 112659 MW; 4264D038E0D225F8 CRC64;
 Query Match 9.3%; Score 122; DB 13; Length 1009;
 Best Local Similarity 21.5%; Pred. No. 0.092; Indels 64; Gaps 7;
 Matches 51; Conservative 28; Mismatches 94;
 QY 11 LTVQLALPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIKILGNQSGFLT 70
 DB 392 LKIALAPTEFTPMRKVLAAGKRVYICKRKAPKAFSSKGTLELI----- 442
 QY 71 KGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQ--LTVFGILTANS 129
 DB 443 -----NNSRYSINDDS--LEIINIRKLBEGSYTCVAENDRGANGTAVLSVTAAT 491
 QY 130 DTHLLQGOSLTLTLESPPSSPSVQCR----- 155
 DB 492 KITLAPSA-----DYTVGENATMQCNASHDPTLDLSYISLNGFPIEFMEDRHVERAI 546
 QY 156 RSPRGNIQGKTLVSQLELDQSGTWTCTVLONQKKEFKIDIVPRASALPAPTPT 212

Db	544	RLP(L)ONDV--GSELLIKNAQLKAGRYCTCTQTIYDMSASADLVVRGP--RGP	PGC 599
RESULT	60		
ID	08HYV1	PRELIMINARY;	PRT; 885 AA.
AC	08HYV1		
DT	01-MAR-2003 (TREMBlrel. 23, Created)		
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)		
DE	glycosylphosphatidylinositol anchor 1 protein (Fragment).		
GN	MDGAL.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kierstein S., Al-Bayati H., Kollers S., Brenig B.;		
RT	"Assignment of the porcine MAM domain containing		
RT	glycosylphosphatidylinositol anchor 1 (mdgal) on chromosome 7q11-13 by		
RL	in situ hybridisation."		
RL	Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.		
EMBL	AL459296; CAD30702.2; -		
GO	GO:0016020; C:membrane; IEA.		
DR	InterPro; IPR008957; FN_III-like.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-1-like.		
DR	InterPro; IPR003598; IG_C2.		
DR	InterPro; IPR009398; MAM_domain.		
Pfam	PF00047; IG_5.		
Pfam	PF00629; MAM_1.		
DR	PRINTS; PR00020; MAMDOMAIN.		
DR	SMART; SM00409; IG_5.		
DR	SMART; SM00408; IGc2_5.		
DR	SMART; SM00137; MAM_1.		
DR	PROSITE; PS00835; IG_LIKE; 5.		
DR	PROSITE; PS50060; MAM_2; 1.		
FT	NON TER		
FT	1		
SQ	SEQUENCE 885 AA; 97766 MW; BC2929D59C3491C5 CRC64;		
Query Match	9.2%; Score 121; DB 6; Length 885;		
Best Local Similarity	26.3%; Pred. No. 0.094; Matches		
Matches	47; Conservative 24; Mismatches 66; Indels 42; Gaps 7.		
QY	36 TVELTCTSQKSIQFHWKNSNQIKLGNQGSFLTKGPKLNDRAISRRLDQGNFPLI 95		
DB	82 TVFLACTYNSNPRAFIWKRGSD-----TLSSQDNG-VDIYEPITYGGAIVL 129		
QY	96 -IKNLKIEDSDTYICEVED-----QKEVQVLVFGLTANSPTLLLGQSITLTLESPPG 148		
DB	130 KLKIDLRPQEVASLTQGVDSGVCIGIPDKAVTLRLTSTTAPAPKL----SVNETLVNVP 185		
QY	149 SSPSVQC-----RSPRGKNIQGGKLTLSVQLELDQSGTTCIVLON 189		
DB	186 ENVTVQCLDGGDPLTQLOWSHGPGPLPGALAQGG-TLSIPSVQARDSGYNYCTATNN 243		
RESULT	61		
ID	08HYV2	PRELIMINARY;	PRT; 886 AA.
AC	08HYV2		
DT	01-MAR-2003 (TREMBlrel. 23, Created)		
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)		
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)		
DE	MAM domain containing glycosylphosphatidylinositol anchor 1		
DE	(Fragment).		
GN	MDGAL.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		

RP SEQUENCE FROM N.A.
RA Kierstein S., Al-Bayati H., Kollers S., Brenig B.;
RT "Assignment of the porcine MAM domain containing
RT glycosylphosphatidylinositol anchor 1 (MDG1) on chromosome 7q11-q13
RT by in situ hybridisation."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ459295; CAD30701.2; -
DR GO: 0016020; C:membrane; IEA.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00047; Ig; 5.
DR Pfam: PF00629; MAM; 1.
DR PRINTS: PRO0020; MAMDOMAIN.
DR SMART: SM00409; Ig; 5.
DR SMART: SM00408; IGC2; 5.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS50835; IG_LIKE; 5.
DR PROSITE: PS50060; MAM_2; 1.
FT NON TER 1
SQ SEQUENCE 886 AA; 98074 MW; B69872711DB9D52 CRC64;

Query Match 9.2%; Score 121; DB 6; Length 886;
Best Local Similarity 26.3%; Pred. No. 0.095;
Matches 47; Conservative 24; Mismatches 66; Indels 42; Gaps 7;

Qy 36 TVELTTCASQKKSIOFHMKNSTQIKILGNQGSFLTKGPSKLNDADSRSLMDQGNPLI 95
Db 83 TVFLRCLTVNSPPARFLTKGSD-----TLSHSQNG-VDIYELPYTGAEVL 130
Qy 96 -IKNLKIEDSDTYICEVED-----QKEVQLVFGLTANSDTHLQGSITLTLESPPG 148
Db 131 KLKLRQEVASLTQVSDGVCIGPKAVTLRLTSTTAPALKL-----SVNETLVNPG 186
Qy 149 SSEPVC-----RRPRGNIGCGKTLISVQLQLDSSGWTCTVLN 189
Db 187 ENTVQCLLOGDPLTLOWSHGPPPLGLALQGG-TLSIPVQARDSGYNNCTATNN 244

RESULT 62
P79921 PRELIMINARY; PRT; 1005 AA.
AC P79921;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Contactin/F3/F11.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Textid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J strain; TISSUE=Brain;
RA Naeata S., Fujita N., Takeuchi K., Watanabe K.;
RT "cDNA cloning and expression of the Xenopus homologue of the neural
RT cell adhesion molecule, contactin (F3/F11).";
RL Zool. Sci. 13:813-820(1997).
DR EMBL: D86505; BAAL3100.1; -
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00041; fn3; 4.
DR Pfam: PF00047; Ig; 6.
DR SMART: SM00060; FN3; 4.
DR SMART: SM00408; IGC2; 5.
DR PROSITE: PS50835; IG_LIKE; 6.
KW Immunoglobulin domain.
SQ SEQUENCE 1005 AA; 11665 MW; 6F1CE811FBD9D7DFE CRC64;

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Query Match          9.1%; Score 120; DB 13; Length 1005;
Best Local Similarity 21.6%; Pred No. 0.14;
Matches 51; Conservative 28; Mismatches 91; Indels 66; Gaps 7;

OY 11 LVLQALLPATQGNKVVLGKGGDTVELTCTASQKSAIQFMKNNSNOIKILNGQSFLLT 70
DB 392 LKILALAPTEFTPPKRVKYLAKGGRVILECKPKAPAKPAPKFSMSGTELLI----- 442
OY 71 KPSKLTNRADSRRLNMQGNFPLIINKLKIEDSTYICEVEDQKEEYQLVFGILTANS 130
DB 443 -----NNSRVSIMDGS--LEITNITKFEDESSYTCFAMENDRGK-----ANS- 481
OY 131 THLLOGSLTLTLEPP-----GSSPSVQCRSPRGKNIQ----- 164
DB 482 TGIYSVTATKTLTLPASNADVTGSENATMOCHASHDPTLELFTWALNGFPIEFKXG 541
OY 165 -----GKTLVSQLELODSCGTWCTVLONQKKEFKIDIVPRASALPAPPTG 212
DB 542 YERAIRNVGSELVIGNKQLIHAGRYTCTAQTIVNSSASADLVVRGP--PGPPGG 595

RESULT 63
ID P70193 PRELIMINARY; PRT; 1091 AA.
AC P70193;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Membrane glycoprotein.
GN LRIG1 OR IMG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96394313; PubMed=8798419;
RA "cDNA cloning of a novel membrane glycoprotein that is expressed
RT specifically in glial cells in the mouse brain LIG-1: A protein with
RL J. Biol. Chem. 271:22522-22527(1996).
DR EMBL: D78572; BAA11416.1; -
DR PIR: A58532; A58532.
DR HSSP: P56276; ITLK.
DR MGD; MGI:107935; Lxlg1.
DR InterPro: IPR007110; IG-1-like.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000463; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00560; LRR_14.
DR Pfam; PF01463; LRRCT_1.
DR Pfam; PF01462; LRRNT_1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SMO0408; IGC2_3.
DR SMART; SMO0082; LRRCT_1.
DR SMART; SMO0013; LRRNT_1.
DR SMART; SMO0369; LRR_Typ_4.
DR PROSITE; PS50835; IG-LIKE; 3.
KM Immunoglobulin domain.
SQ SEQUENCE 1091 AA; 119283 MW; A13D0866CE4C203D CRC64;

Query Match          9.1%; Score 120; DB 11; Length 1091;
Best Local Similarity 22.3%; Pred No. 0.15;
Matches 60; Conservative 40; Mismatches 103; Indels 66; Gaps 10;

OY 14 LQALLPATQGNKVVLGKGGDTVELTCTASQKSAIQFMKNNSNOIKILNGQSFLLT 73
DB 595 LTVNVLPSTFKIPHDIAIRGTGTARLECAATGCHNPQIAWQKDG-----IDFP 643

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OY 74 SKLNRADSRRLNMQGNFPLIINKLKIEDSTYICEVEDQKEEYQLVFGILTANSPTHL 133
DB 644 A-----ARERMMVMPDDVFFITVDKIDMGVSTCAONASGV-----SANATITLV 691
OY 134 LOGSLTLTLES---PRSSPSVQCR-----SPRGKNIQGGKTLSS----- 170
DB 692 LETSLAVPLEDRVVTYGETVAFQCKATGSPRTITLWKGRPLSLTERHHFTPGNQLLV 751
OY 171 VSQLELODSCGTWCTVLONQKKEFKIDIVPRASALPAPPTGSLPDPOTASALPDP 229
DB 752 VQNMWIDAGRYTCE-MSNPGLTE-----FAHSQSLIFTPGCRKRGDTVGIF----- 798
OY 230 ASALPALAVSFLIGLGAGVCLARTR 258
DB 799 -----TIAVCSITVLSLWVWCITTYOR 821

RESULT 64
ID O97394 PRELIMINARY; PRT; 2222 AA.
AC O97394;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SIDEKICK protein (CG5227-PA) (CG5227-PB).
GN SDK OR BCDNA.LD22322 OR CG5227.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen D.N.T., Liu Y., Litsky M.L., Reinke R.
RT "Sidekick, a member of the immunoglobulin superfamily, is required for
RT pattern formation in the Drosophila eye."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

(2)
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davaport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostlin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matcel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

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RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Ye R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celisner S.E.,
 RA Champ M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harria N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutnak F., Richter J.,
 RA Whitfield E.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
 RA Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88578; AAD09632.1; -;
 DR EMBL; AE003418; AAF4541.3; -;
 DR PIR; T13924; T13924.
 DR HSP; P56276; TLK.
 DR Flybase; FB00021764; sdk.
 DR InterPro; IPR003962; Fm11 subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF000041; fn3; 13.
 DR Pfam; PF000047; ig; 5.
 DR PRINTS; PR00014; FNTYPE11.
 DR SMART; SM00060; FN3; 13.
 DR SMART; SM00408; IGC2; 4.
 DR PROSITE; PS50835; IG LIKE; 5.
 KW Immunoglobulin domain; Repeat.
 KW SEQUENCE 2222 AA; 246174 MW; 18853CCAF98DB2 CRC64;
 Query Match 9.1%; Score 120; DB 5; Length 2222;
 Best Local Similarity 24.0%; Pred. No. 0.39;
 Matches 54; Conservative 30; Mismatches 85; Indels 56; Gaps 11;
 QY 26 NKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKILGNGSFLTKGPSKLNDRADRRS 85
 DB 463 NVTLADGDADATISGRAVSPNPNTWTWNETQLVDI-----SSRVQ 503
 QY 86 LMDQGNFLIKNLKIEDSDTYIC-----EVEDQKEVQLVFGLT---ANSPTHLIQG 137
 DB 504 ILSEGD--LLISNRSVADAPLYICVRANEGSVAAEAVLSLVVTOIIQPPVDTVLIG- 560
 QY 138 SLTTLSPGSSPSV-----QCRSPKGN---IQGKTLVSQLELDQSGTWT 183
 DB 561 -LTAATLQCKVSSDPSVPYNIDVREGQSTPISNSQRIQVADQLRIQAVRASDVGSYA 619
 QY 184 CTVAQ---NKKVFEKIDIVRAALAPPTG---SALPDPQTSS 222
 DB 620 CVVTSFGNETRAA-RLSVTL---ELPPPSNVKVERLPEPQAS 659
 RESULT 65
 Q9JLM2 PRELIMINARY; PRT; 311 AA.
 AC Q9JLM2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE NK cell receptor 2B4;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20260986; PubMed=10803843;
 RA Kumaresan P.R., Stepp S.E., Bennett M., Kumar V., Mathew P.A.;
 RT "Molecular cloning of transmembrane and soluble forms of a novel rat
 natural killer cell receptor related to 2B4.";
 RL Immunogenetics 51:306-313(2000).
 DR EMBL; AF156989; AAF71162.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR SMART; SM00409; IG; 1.
 KW Receptor.
 KW SEQUENCE 311 AA; 35300 MW; 5A527D22D2565772 CRC64;
 Query Match 9.1%; Score 119.5; DB 11; Length 311;
 Best Local Similarity 22.4%; Pred. No. 0.033;
 Matches 65; Conservative 43; Mismatches 95; Indels 87; Gaps 14;
 QY 12 LVTLALLPATQG-----NKVVLGKGGDTVELTCTASQKSIQFHMKNNOIKILGNG 65
 DB 6 VLTLFLRLRAHQGDCASSSEVLGSGKPYRLRPSNIOAKHVSIEWK-----KTHQ 60
 QY 66 GSEFLTKGPSKLN-DRADRRSL-----MDQGNFLIKNLKIEDSDTYICEVDQK- 115
 DB 61 -----QTPQIVWDTLDNNFNMCSDIYGFESENFALSIKSLKNDSGHYLLLEINQNG 115
 QY 116 ----BEVQLLVGELTANSPTHL-LOQSILTLSPGSSPSVQCSPPGKNI-----OG 165
 DB 116 IVCTKNFQMLIPDPV--ETPHLVQG-----TLNANGTQLSLSCFVPKDDVSVLYRG 168
 QY 166 GKTLG-----VSQLELDQSGTWTCTVLAQKKVEFIDIVPRASALPAPPTGSALPD 217
 DB 169 SMILSNQRYGTWENTDASSLHTTYCNVSN-----KAS----- 202
 QY 218 POTASALPPPPASALPALAVISPLGLGLVA-----CYLART 258
 DB 203 -WANHTLTSPQSQSVSKENVLPFVWSIGILVYFPGHAIIDGCVNRRK 251
 RESULT 66
 Q9M6V2 PRELIMINARY; PRT; 352 AA.
 ID Q9M6V2;
 AC Q9M6V2;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Neurotactin-L.
 GN NTRA-L.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brunnendorff T.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99264333; PubMed=10330412;
 RA Marg A., Strim P., Spaltmann F., Plagege A., Kauselmann G., Buck F.,
 RA Rathjen F.G., Brunnendorff T.;
 RT "Neurotactin, A novel neurite outgrowth-promoting Ig-1like protein
 that interacts with CBP-1 and LAMP.";
 RL J. Cell Biol. 145:865-876(1999).

DR EMBL: AJ132999; CAB4446.1; -
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00408; IGc2; 2.
DR PROSITE: PS50835; IG_LIKE; 3.
DR Immunoglobulin domain.
KW SEQUENCE 352 AA; 37944 MW; B0FA99F295FDF8FA0 CRC64;

Query Match 9.0%; Score 119; DB 13; Length 352;
Best Local Similarity 22.1%; Pred. No. 0.042;

Matches 51; Conservative 40; Mismatches 90; Indels 50; Gaps 10;

QY 20 PAATGNKVVLCGGKDTVELTCTASQKKSIOFHKNSNOIKILGNQSFILTKRPSKLNDR 79
DB 39 PGAAADSLV--RKDDTVLRCYLEDGAS-KGAMLNRSIIIFAG-----SDK 82
QY 80 --ADSRSL--WDQGNFPLIIKNLKIEDSDTYICEVDQKE-----EVQLLVFGL 125
DB 83 MSVDPKVSIAATANRRREYSLQIDVDVTDGPTGCVQGHPRTHVHLTVQVSPKIPRI 142
QY 126 TANSPTHLLOQSLLTLIESPPGSSPVQCR--SPRGNIQGGKTLVSQLELDGSGTWT 183
DB 143 --SSDIVNEGSMNTLVCLATGKPEPSISWRHISPAKPFESGGYLDYIGITRDQAGEYE 200
QY 184 CTV--LONOKKVEFKIDIVPRASALPAPPT-----GSALPDP 218
DB 201 CSAENDSVDPVKVKKVTVNFAPTTIGELKSGVMIGNGLIRCEGAVPAP 251

RESULT 67

Q44924 PRELIMINARY; PRT; 1395 AA.

AC 044924:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ROUNDABOUT 1.
GN ROBO OR ROBO1 OR CG13521.
OS Drosophila melanogaster (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98117249; PubMed=9458045;
RA Klad T., Brose K., Mitchell K.J., Felter R.D., Tessier-Lavigne M.,
RA Goodman C.S., Tear G.;
RT "Roundabout controls axon crossing of the CNS midline and defines a
RT novel subfamily of evolutionarily conserved guidance receptors.";
RL Cell 92:205-215(1998).
DR EMBL: AF040989; AAC38849.1; -
DR HSSP; P56276; 1TLK.
DR FLYBase; FBgn0005631; robo.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR GO: GO:0007411; P:axon guidance; IMP.
DR InterPro: IPR003962; FN111.sudd.
DR InterPro: IPR003961; FN_111.
DR InterPro: IPR008957; FN_111-1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003598; IG_c2.
DR Pfam; PF00047; fn3; 3.
DR Pfam; PF00047; Ig_3.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00408; IGc2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 1395 AA; 151778 MW; B820E234A5218983 CRC64;

Query Match 9.0%; Score 119; DB 5; Length 1395;
Best Local Similarity 25.8%; Pred. No. 0.26;

Matches 59; Conservative 24; Mismatches 94; Indels 52; Gaps 9;

QY 26 NKVVLGKKGDVVELTCTASQKKSIOFHKNSNOIKILGNQSFILTKRPSKLNDRADRRS 85
DB 353 NKKV-GLNG-VVOLPCNAGNPSPSVFWTK-----EGVSTLMFPNSSHGR 395
QY 86 LMDQGNFPLIIKNLKIEDSDTYICEVDQKEVQLLVFGLTANSDTH---LLQGSLLTLT 142
DB 396 QYVADGTLQITTDVROEDEGYVCSAFSVDSITRVFLQVSSVDERPPPIIQTGPANQT 455
QY 143 LESPSSSPVQCR-----SPRGK-----NIQGGKTLVSQLELDGSGTWT 183
DB 456 L--PKGSVALTPCATGNPSPRIKPFHDGAVQAGNRYSIIGSSSLRVDDLQSDSGTYT 513
QY 184 CTVLQONKVEFKIDIVPRASALPAPPTGSA---LDPQTSALPDP 228
DB 514 CTASGERGETSW-----AATLVKRGSTSLHRAADPSTYPAPPGTP 555

RESULT 68

Q8AW79 PRELIMINARY; PRT; 276 AA.

AC Q8AW79:
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SI.dz125073.8.1 (Novel immune-type receptor 1.8, variant 1)
DE (Fragment).
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Garner P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL591405; CAD58990.1; -
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; IG_1like.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
FT NON TER 276
SQ SEQUENCE 276 AA; 30650 MW; 13CAB6090CEC660 CRC64;

Query Match 9.0%; Score 118.5; DB 13; Length 276;
Best Local Similarity 24.3%; Pred. No. 0.034;
Matches 53; Conservative 26; Mismatches 72; Indels 67; Gaps 9;

QY 24 QGNKVVLCGGKDTVELTCTASQKKSIOFHKNSNOIKILGNQSFILTKRPSKLNDR 73
DB 21 QENNKVLVQAGEDVNLCTSPNMQLSTAMFKATADKTLQIAYN--LFTTKSPIMNNV 78
QY 74 SKLNDRADRRSRLMDQGNFPLIIKNLKIEDSDTYICEVDQKEVQLLVFGL-----T 126
DB 79 EKQND-----VNVIIIEGYFNLITLKTNPDSATYYCV-----SSYEAIGMGLSRLIVRD 130
QY 127 ANSDPTHLLOQSLLTLIESPPGSSPVQCR-----LSPVQLLVFGL 155
DB 131 AATDRNRTLQSLDITVD--PGDSVNLQCSIPTESGAGHSIYFKQSGDSEGVLYTKG 188
QY 156 -RSPRGNIQGGKTLVSQLELDGSGTWTCTV 186
DB 189 ERNRCNKAASSETQSCVYSLHKNNISRSPTGIYYCAV 226

RESULT 69
Q8AW80 PRELIMINARY; PRT; 278 AA.
ID Q8AW80

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AC 08AM80;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE S1:dz125j23.8.2 (Novel immune-type receptor 1.8, variant 2)
DE (Fragment).
GN NTR1.8.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Garner P.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL591405; CAD58989.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG_LIKE; 2.
KM Receptor.
FT NON TER.
SQ SEQUENCE 278 AA; 278
EAB558B7413BF5EE CRC64;

Query Match 9.0%; Score 118.5; DB 13; Length 278;
Best Local Similarity 24.3%; Pred. No. 0.034;
Matches 53; Conservative 26; Mismatches 72; Indels 67; Gaps 9;

QY 24 QGNVTVLGGKGDVLTCTASQKSIQPHW-----KSNQKILGNQGSFLTGP----- 73
ID 080224 PRELIMINARY; PRT; 584 AA.
AC 09Y3Y8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKZP56411922.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Wambut R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049946; CAB43220.1; -
DR PIR; T08678; T08678.
DR HSP; P56276; ITLK.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_6.
DR SMART; SM00408; IGc2; 4.

DB 133 AATDRNRTLHQLSLIDTVD--PGDSVNLQCSIFTESCAGDSHWFKQSGDSEGLVYTKG 190
QY 127 ANSDTHLLQGSLTTLTLESPGSSPVOC----- 155
ID 156 -RSPRGKNIQCKT-----LSVQLQDPSGTCITCV 186
DB 191 ERNGRCNKAASETQSCVSYSLKKNNISRPDTGIYCAV 228

RESULT 70
QY3Y8
ID 09Y3Y8 PRELIMINARY; PRT; 584 AA.
AC 09Y3Y8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKZP56411922.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RA Wambut R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049946; CAB43220.1; -
DR PIR; T08678; T08678.
DR HSP; P56276; ITLK.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_6.
DR SMART; SM00408; IGc2; 4.

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DR PROSITE; PS50835; IG_LIKE; 6.
KM Hypothetical protein; Immunoglobulin domain.
FT NON TER.
SQ SEQUENCE 584 AA; 63918 MW; 9C75943922BADCA9 CRC64;

Query Match 9.0%; Score 118.5; DB 4; Length 584;
Best Local Similarity 21.2%; Pred. No. 0.091;
Matches 59; Conservative 38; Mismatches 90; Indels 91; Gaps 12;

QY 32 KKGDTVELTC-----TASQKSIQPHWKNQKILGNQGSFLT-----KQPSKND-R 79
ID 165 QKSDSGNYTCLVRNSAGEDRKTVWIH-VVWQPKINGNPNPTTVVEIAAGSRKLDCK 223
DB 224 AGIPLPRVLMAFPPEGVLPARYGNRTVHNGSLDLSLRKSDSVOLVCARNEGGA 283
QY 119 QLL-----VFGLTANSDFHLLQGSLTTLTLESPGSSPVOCSPRGKNIQGG 166
DB 284 RLILQLTVLEPMEKPTFHPDPISEKTTAMAGHTISLNGSAGCTPESLWVWLPNGTDLQSG 343
QY 167 KTLT-----VSQLELDQSGTWTCTVLQN-----QKVEFKIDIVPRAS----- 204
DB 344 QOLQREYHKADGMLHISGLSVDAQAYRC-VARNAAGHTERLVSLKVLKPEASKQYHNL 402
QY 205 -----ALPAPPTGSA-----LPPQT 220
DB 403 VSIINGETIKLPCTPPGAGGRFSWTLPNGMHLGEPQT 440

RESULT 71
Q80Z24
ID 080224 PRELIMINARY; PRT; 348 AA.
AC 080224;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Neurotactin.
GN NTRA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Balb c; TISSUE=Brain;
RA Mery A., Stim P., Spaltmann F., Plage A., Kauselmann G., Buck F.,
RA Rathjen F.G., Brummendorf T.;
RT "Neurotactin, a novel neurite outgrowth-promoting Ig-like protein
RT that interacts with CEP-1 and LAMP."
RL J. Cell Biol. 4:865-876(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Balb c; TISSUE=Brain;
RA Schaefer M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ487032; CAD31699.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 348 AA; 37900 MW; 30520A146A9FA198 CRC64;

Query Match 9.0%; Score 118; DB 11; Length 348;
Best Local Similarity 23.0%; Pred. No. 0.051;
Matches 53; Conservative 34; Mismatches 95; Indels 48; Gaps 10;

QY 20 PAATQGNKTVLGGKGDVLTCTASQKSIQPHWKNQKILGNQGSFLTGP---SK 75
DB 35 PMAAVDNMLV--RKGDVAVLCVLEDDGAS-KGAWLNRSSIIFAG--GDKWSVDPKVSIST 89

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Oy 76 LNDNRASRSLMDGPNPLITKNLKIEDSPDYICEVEDOKKEVOLLVFGLTA----- 127
Db 90 LNKR-----DYLQIQNVNTVDGPTTCSVQIQHPRTMQV-LTVQVPPKTYD 137
Oy 128 -NSDTHLLQSGSLTTLTSPSSPSVOCR--SPRKNIQGGKTLVSQLELQDSGTWC 184
Db 138 ISNDWTINEGNTVLTCLATGKPEPVIWMHISPAKFPENGQYLDIGIRDQAGEYEC 197
Oy 185 TV-----LQNGKVEFKDIYPRASALAPPF-----GSALDPP 218
Db 198 SAENDVSPDYKVRVIVNFAPTIOEIKSGVTTPGSRGLRCEGAGVPP 247

RESULT 72
Oy 09VP08 PRELIMINARY; PRT; 403 AA.
AC 09VP08;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG166 protein.
GN CG166.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekstra M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake R.G., Champagne M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.C.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA de Pabloe B., Delcher A., Deng Z., Nays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Lang D., Lai Z.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Platan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svyrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

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RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorett V., Doup L.E., Doyle C., Dresnek D., Fartan D.,
RA Ferreira S., Frise E., Galle R.F., Gary N.S., George R.A.,
RA Gonzalez M., Houck J., Hoekstra M., Hostin D., Howland T.J.,
RA Ibegwan C., Jaitani M., Kruse D., Li P., Maltel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Patel S., Pfeiffer B.,
RA Pacle J., Paragas V., Park S., Puri V., Richards S., Scheeler F.,
RA Phouanavong S., Platan G.S., Puri V., Svirskas R., Tector C., Tyler D.,
RA Stapleton M., Strong R., Svyrkas R., Tector C., Turner R.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutnack F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003595; AF51754.2; -
DR FlyBase; FBgn0037107; CG166.
DR InterPro; IPR001064; CysTalin.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IGc2_3.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR KEGG; K04901; Drosophila melanogaster.
SQ SEQUENCE 403 AA; 45747 MW; 429C1039F539F76D CRC64;

Query Match 9.0%; Score 118; DB 5; Length 403;
Best Local Similarity 23.9%; Pred. No. 0.062;
Matches 45; Conservative 34; Mismatches 75; Indels 34; Gaps 9;

Oy 27 KVVVGKGGDVTVELTCTASQKKSIOFHKNSNQIKLNGSGFLTGKSPKLNDRASRSL 86
Db 33 KVIY---GTEILPCKQKNGSPFLMKRS-----SVLTAGHLKIT--RDQFKI 78
Oy 87 WDQGNFPLITKNLKIEDSDTYICEVEDOKKE-----VQLLV---FGLTNSDTHLLQGO 137
Db 79 --VDQVNIQNGVTVQDAGDYICQLGQENRDQVHTVEILVPTLRALPHNGVTVARKS 136
Oy 138 SLTTLTSPSSPSV-----QSRPKNIQGGKTLVSQLELQDSGTWCITVLQNGK 191
Db 137 TVTLECAASNPVPTTFWFKDVFSGP--THLSDSTLILEVDRHAGTYQCSA-DNGV 193
Oy 192 KVEFKIDI 199
Db 194 KDRYSMDI 201

RESULT 73
Oy 09D221 PRELIMINARY; PRT; 577 AA.
AC 09D221;

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DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE 9130012D09RIK protein.
 GN 9130012D09RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
 RA Akazawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kodera K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gisi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guarnieri S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima U., Mazzarelli J., Mombaerts P.,
 RA Norde P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohatsu S.,
 RA Hayaishi Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 DR EMBL: AK018613; BAB1107.1; -
 DR MGD: MGI:1918851; 9130012D09RIK.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG C2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00408; IGC2; 2.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR KEGG: Immnoglobulin domain
 SO SEQUENCE 577 AA; 63444 MW; C3470C7B60FB8B2B CRC64;
 Query Match 9.0%; Score 118; DB 11; Length 577;
 Best Local Similarity 22.5%; Pred. No. 0.099;
 Matches 60; Conservative 42; Mismatches 91; Indels 74; Gaps 12;
 QY 13 VLQALPAPATQGN---KVLGKGDTELTCTASQKSIQPFWMKNSNQIKLNGSGF 68
 DB 227 VVKQVLEKVTAPNIEPFTLALVENATSVTLCTKSHQR-VGVNM-----F 271
 QY 69 LTKGPEKLNDRADRSRLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQLVFGITAN 128
 DB 272 LKQGPLRPSPDRL---TLSSQ-NRTLTHGLGRDIDGPECEVNMNSQARSVPKLTIN 326
 QY 129 ---SDTHLQG--QSLTLTLESPPGSSPSVQCRS-----PRGNKIQGKTLV 171
 DB 327 YGPDQVEITQGPASGVSTIEAMLNSSLTLYCRADSIPGARVQWTHHSKVLDDGELSI 366
 QY 172 SQLELDSDGWTCTVQLQNKVEFKIDIVPRASALPAPPGSALPDQGTASAL---PDP 228
 DB 387 EALRQEHQGIYSTCTSSND-----VTGLA---RSASVLMVVGQLQ 422
 QY 229 AASALPALA-----VISFLGLGLG 249
 DB 423 SSSMSFGAIGIVIGIIVATLALGLG 449

ID 080V42 PRELIMINARY; PRT; 577 AA.
 AC 080V42;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE 9130012D09RIK protein.
 GN 9130012D09RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R.L., Feilgold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Mullany S.J.,
 RA Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Strausberg R.;
 DR EMBL: BC049361; AAH49361.1; -
 DR Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG C2.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; IG; 4.
 DR SMART: SM00408; IGC2; 4.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR KEGG: Immnoglobulin domain
 SO SEQUENCE 577 AA; 63426 MW; EF52B146A50EB871 CRC64;
 Query Match 9.0%; Score 118; DB 11; Length 577;
 Best Local Similarity 22.5%; Pred. No. 0.099;
 Matches 60; Conservative 42; Mismatches 91; Indels 74; Gaps 12;
 QY 13 VLQALPAPATQGN---KVLGKGDTELTCTASQKSIQPFWMKNSNQIKLNGSGF 68
 DB 227 VVKQVLEKVTAPNIEPFTLALVENATSVTLCTKSHQR-VGVNM-----F 271
 QY 69 LTKGPEKLNDRADRSRLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEYQLVFGITAN 128
 DB 272 LKQGPLRPSPDRL---TLSSQ-NRTLTHGLGRDIDGPECEVNMNSQARSVPKLTIN 326
 QY 129 ---SDTHLQG--QSLTLTLESPPGSSPSVQCRS-----PRGNKIQGKTLV 171
 DB 327 YGPDQVEITQGPASGVSTIEAMLNSSLTLYCRADSIPGARVQWTHHSKVLDDGELSI 366
 QY 172 SQLELDSDGWTCTVQLQNKVEFKIDIVPRASALPAPPGSALPDQGTASAL---PDP 228
 DB 387 EALRQEHQGIYSTCTSSND-----VTGLA---RSASVLMVVGQLQ 422
 QY 229 AASALPALA-----VISFLGLGLG 249

Db 423 SSSMPCAGIAGIVIGILVAMALATGLG 449

RESULT 75

Q9W213 PRELIMINARY; PRT; 1395 AA.

AC Q9W213; (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE CG13521 Protein.

GN ROBO OR CG13521.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkeley;

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X., Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotlier P., Butte K.C., Buzan D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dea Pablos B., Delcher A., Deng Z., Dey I., Dietz S.M., Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W., Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C., Jaisl M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.H., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*."

RL Science 287:2185-2195 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D., Batzon J., Beeson K.Y., Buzan D.A., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Ferritara S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez F., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwan C., Jaisl M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J., Pacle J.M., Paragas V., Park S., Patel S., Pfeiffer B., Pounanavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirkas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

RT "Sequencing of *Drosophila melanogaster* genome."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Krommiller B., Marshall B., Milburn G.H., Richter J., Russo S., Searle S.M.U., Smith E., Shu S., Smutnack F., Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of *Drosophila melanogaster* genome."

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003458; AM471113.1; -.

DR HSSP; P56276; ITLK.

DR FlyBase; FBgn005631; robo.

DR GO; GO:0005886; C:plasma membrane; IDA.

DR GO; GO:0007411; P:axon guidance; IMP.

DR InterPro; IPR003962; PiliI subd.

DR InterPro; IPR003961; FN_III.

DR InterPro; IPR008957; FN_III-like.

DR InterPro; IPR007110; IG_III-like.

DR Pfam; PF00041; fn3; 3.

DR Pfam; PF00041; fn3; 5.

DR PRINTS; PR00014; FNTYPEIII.

DR PROSITE; PS50835; IG_LIKE; 5.

KW Repeat.

SQ SEQUENCE 1395 AA; 151759 MW; 25CED7DEB44F13F0 CRC64;

Query Match 9.08; Score 118; DB 5; Length 1395;

Best Local Similarity 25.3%; Pred. No. 0.31; Indels 52; Gaps 10;

Matches 58; Conservative 25; Mismatches 94;

Qy 26 NKVVLGKKGPVETLTASQKSIQFMKNSNQIKLGNOSPLTKPSKLNDRADSR 85

Db 353 NKKV-GLVG-VQVLPQCAASNPSPVMTKEGVSTLM-----FNSHGHQVAAVG--- 402

Qy 86 LMDQGNPPLIKKLIKEDSTTYICEVDQKEVQLVFGITANSDDH---LLQCSGLTT 142

Db 403 -----TLITDTRQDEGVYVCSAFSVSDSTVRFVLVSSLDERPPIIQIGPANOT 455

Qy 143 LESPSSPSPVOCR-----SPRGK-----NTQGGKTLVLSOLELDGSGTWT 183

Db 456 L-PKSVATLPCCATNPSPRIKMFHDGAVQAGNRYSLIIGSSLVVDLQSDSGITT 513

Qy 184 CTVLQNKQKVEFKIDIVPRASALPAPPTGSA---LPDPQTASALPDP 228

Db 514 CTASGGERGERSW-----AATLVEKRGSTSLHRADPETYAPPTGP 555

RESULT 76

Q8IRV9 PRELIMINARY; PRT; 4117 AA.

AC Q8IRV9;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE CG7981-PC.

GN TROL OR EG:BACR2583.11 OR CG7981.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

CC Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

OX [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.;

NCBI_TaxID=7227;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoinkins R.A., Galie R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blake R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Beeson P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 Butte K.C., Buesam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablo B., Delecher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hoeft D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 Jaisl M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusaker D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhou Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 [2]
 SEQUENCE FROM N.A.
 Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Buesam D.A.,
 Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Dou P.L.E., Doyle C., Dresnek D., Fartan D.,
 Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
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 Ibegwam C., Jaisl M., Kruse D., Li P., Mattei B., Moshrefi A.,
 McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 Phanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 "Sequencing of *Drosophila melanogaster* genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 SEQUENCE FROM N.A.
 Miera S., Crosby W.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Hirdcey P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 Seearle S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of *Drosophila melanogaster* genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE FROM N.A.

Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 RA FlyBase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003424; AAF45786.3; -
 DR HSSP; P00740; IEDM
 DR FlyBase; FBgn0001402; trol.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0006306; P:DNA methylation; IEA.
 DR InterPro; IPR001525; C5 DNA meth.
 DR InterPro; IPR008985; CofA-like lec_g1.
 DR InterPro; IPR007742; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000034; laminin_B.
 DR InterPro; IPR002049; laminin_EGF.
 DR InterPro; IPR001791; laminin_G.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00047; Ig_12.
 DR Pfam; PF00052; laminin_B_3.
 DR Pfam; PF00053; laminin_EGF_2.
 DR Pfam; PF00054; laminin_G_3.
 DR Pfam; PF00057; Id1_recept_a; 23.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR SMART; SM00180; EGF_lam; 9.
 DR SMART; SM00409; IG_12.
 DR SMART; SM00408; IG2_12.
 DR SMART; SM00281; LamB; 3.
 DR SMART; SM00282; LamG; 3.
 DR SMART; SM00192; LDLA; 23.
 DR PROSITE; PS00094; C5_MTASE_1; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS50835; IG LIKE; 11.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 7.
 DR PROSITE; PS50025; LAM G DOMAIN; 3.
 DR PROSITE; PS01209; LDLA_1; 20.
 DR PROSITE; PS50068; LDLA_2; 23.
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 DR Immunoglobulin domain; Laminin EGF-like domain.
 SQ SEQUENCE 4179 AA; 461782 MW; 47804277D0914E63 CRC64;
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 Best Local Similarity 23.1%; Pred. No. 1.3; Indels 64; Gaps 9;
 Matches 45; Conservative 31; Mismatches 55;
 Oy 32 KKGPVTLTCTASQ-----KKSIOFMKNSNOIKILGNQSFLLKPSKLNDRADSR 85
 Db 3193 REGNIDLOCTVVDQYVRAQDNVFRWFRDD-----RRPLNNMATDQ-- 3227
 Oy 86 LMDQGNFPLIIKNIKILKEDSDTYICEVD-----QKEVVQLVREGLT---NSDTHL-- 133
 Db 3238 -----ILVITNLRPEDAGRYICNSYDVRCQQLPEVSIDLQVLTATPPNSPIYLPQ 3290
 Oy 134 --LQGSGLTTLBEP-----FGSSPSVQCS-----PRKNT-OGGKTL 169
 Db 3291 LPAASRYSLKLDQSSNLRAGSTDVCEYSDDTYTVDVWERSDGAFLSNVRQVGNRL 3350
 Oy 170 SVSGLQLQDSGTWC 184
 Db 3351 VISVSSDAGNYVC 3365
 RESULT 78
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 AC Q8MPN3;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Perlecan (CG7981-PD).
 GN TROLO OR EG:BACR25B3.11 OR CG7981.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN
 RP SEQUENCE FROM N.A.
 RA Voigt A.;
 RT "Perlecan participates in proliferation activation of quiescent
 RT Drosophila neuroblasts";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazew R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Boutan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Dey A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielloni A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jhalili M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weissbrock G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ceiniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorset V., Doup L.E., Doyle C., Dresnek D., Fatfan D.,
 RA Ferrera S., Frise E., Galle R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jhalili M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 RA Paclet J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanemvong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AA487018; CND31650.1; -;
 DR EMBL; AE003424; AAN09079.1; -;
 DR FlyBase; FBgn0001402; trol.
 DR GO; GO:0003677; F.DNA binding; IEA.
 DR GO; GO:0005198; F.structural molecule activity; IEA.
 DR GO; GO:0006306; P.DNA methylation; IEA.
 DR InterPro; IPR001525; C5_DNA_meth.
 DR InterPro; IPR008985; CofA_like_1ec_g1.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000049; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00067; Ig_13.
 DR Pfam; PF00052; Laminin_B_3.
 DR Pfam; PF00053; Laminin_EGF_2.
 DR Pfam; PF00054; Laminin_G_3.
 DR Pfam; PF00057; ldl_recept_a; 23.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR ProDom; PD003031; Laminin_B_3.
 DR SMART; SM00180; EGF_Lam; 8.
 DR SMART; SM00409; Ig_13.
 DR SMART; SM00408; IGC2_13.
 DR SMART; SM00281; LAMB; 3.
 DR SMART; SM00282; LAMG; 3.
 DR SMART; SM00192; LDLa; 23.
 DR PROSITE; PS00094; C5_WTASE_1; 1.
 DR PROSITE; PS00022; EGF_1; 10.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS00835; IG_Like; 12.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 7.
 DR PROSITE; PS0025; LAM_G_DOMAIN; 3.
 DR PROSITE; PS01209; LDLRA_1; 20.
 DR PROSITE; PS0068; LDLRA_2; 23.
 DR PROSITE; PS00030; RRM_RNP_1; 1..
 KM Immunoglobulin domain.
 SQ SEQUENCE 4223 AA; 466919 MW; 31D7C2B5C9B1D2E0 CRC64;
 Query Match 9.0%; Score 118; DB 5; Length 4223;
 Best Local Similarity 23.1%; Pred. No. 1.3;
 Matches 45; Conservative 31; Mismatches 55; Indels 64; Gaps 9;
 Qy 32 KKSDYELVCTASQ-----KKSIOFHWKNSNOKITLGNCGSFLTGPSKLNDRADSRRS 85
 Db 3237 RRSNNIQLQCTVTDYGVRAQDVERNWRPDD-----RRPLENNARKTDSQ-- 3281
 Qy 86 LMDQGNFPLIKNLKTIKSDTYICEVED-----QKEEVOLLVGLTA---NSDTHL--- 133

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Db 3282 -----ILVLTNLRPEDAGRYCNSVDVDRGQQLPEVSIQLQVLTATPPNPSPYLTPPQ 3334
Qy 134 --LOGSITLTLSES-----PGSSSVQCRS-----PRGKNT-QGKTL 169
Db 3335 LPASRDYSLKLDQSSNLRAGESTDEVCSSDDTYTDVWERSDGAFLSNVVRQVGNRL 3394
Qy 170 SVSOLELQDSGTWTC 184
Db 3395 VISNVSPSDAGNYVC 3409

RESULT 79
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AC Q23550, Q23020, Q27232; 01. Created)
DT 01-NOV-1996 (TREMBlrel. 01.
DT 01-NOV-1998 (TREMBlrel. 08. Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25. Last annotation update)
DE UNC-22 protein.
GN UNC-22 OR ZK617.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S., Harris B.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 784-6831 FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=90044042; PubMed=2812002;
RA Benian G.M., Kilt J.E., Neckelmann N., Moerman D.G., Waterson R.H.;
RT "Sequence of an unusually large protein implicated in regulation of
RT myosin activity in C. elegans.";
RL Nature 342:45-50(1989).
RN [3]
RP SEQUENCE OF 784-6831 FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=9387664; PubMed=8397135;
RA "Additional sequence complexity in the muscle gene, unc-22, and its
RT encoded protein, twitchin, of Caenorhabditis elegans.";
RL Genetics 134:1097-1104(1993).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=a;
CC Isoleid=Q23550-1; Sequence=Displayed;
CC Note=No experimental confirmation available;
CC Name=b;
CC Isoleid=Q23551-1; Sequence=External;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z73897; CA98064.1; -.
DR EMBL; Z73899; CA98081.1; JOINED.
DR EMBL; Z73897; CA98081.1; JOINED.
DR EMBL; X15423; CA93463.1; -.
DR PIR; A88852; A88852.
DR PIR; S57242; S57242.
DR HSP; O63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004812; F:rRNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR000719; Prot_kinase.

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DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR001412; RNA-synt_1.
DR Pfam; PF00041; fn3; 31.
DR Pfam; PF00047; ig; 21.
DR Pfam; PF00069; kinase; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00060; FN3; 27.
DR SMART; SM00408; IGc2; 6.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PROSITE; PS50835; IG-LIKE; 21.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Alternative splicing;
KW Immunoglobulin domain; Kinase; Repeat;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 6831 AA; 752596 MW; 6CADB032963A52E1 CRC64;

Query Match 9.0%; Score 118; DB 5; Length 6831;
Best Local Similarity 23.3%; Pred. No. 2.5;
Matches 58; Conservative 36; Mismatches 87; Indels 68; Gaps 12;

Qy 8 RHLLVQLALPAPATGKVKVYLGKGDYELTCTAQQKSIGPHWKNQSIKILGNQGS 67
Db RHFTFV-----PKSQ--KV--NESDLATLETVDVNDKAEVVMHMGKRKIDIDGVK-- 1032
Qy 68 FLTKGPSKLNDRADRSRLMDQGNFPLIKLKIETSDTYICEVEDQKEEYQVLVFG-- 124
Db -----KRVSSNRKR-----LIINGARIEDGEYKCTTKDRITMAQLIVDAKNK 1077
Qy 125 -LTNSDTHLQGSITLTLSPSPSSPVQCRSPRKNTQ---GK-----TLS 170
Db 1078 FIVALKDTEVLEKQDVLTMCQTQKTGPIWFRN--GKQISSMVGKFEETQSRNGHTLTK 1135
Qy 171 VSQLELDS-----GTWCTYLVQND-----KVEFKIDIVPRASALPAP 210
Db 1136 IGIENKAEADVYEIDAGLRGSCNVTLAEKRPILMWKPKIEAKAG-EPCVAVKVPFOI 1194
Qy 211 TGSALPDPQ 219
Db 1195 KGTGRGDPK 1203

RESULT 80
Q23551 PRELIMINARY; PRT: 7158 AA.
AC Q23551;
DT 01-NOV-1996 (TREMBlrel. 01. Created)
DT 01-JUN-2003 (TREMBlrel. 24. Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25. Last annotation update)
DE Hypothetical protein ZK617.1b (C. elegans UNC-22 protein)
DE (Corresponding sequence ZK617.1b).
GN ZK617.1b OR UNC-22.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
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RN [1]
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RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA White S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

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RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., McKlos G.L.G.,
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 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RA Celinker S.E., Adams M.D., Kronmiller B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Carlson J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Houston D., Howland T.J.,
 RA Ibegwan C., Jaitani M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoumanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RA Miara S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bernier B., Carlson J.W., Celinker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnicki F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003599; AAF51887.2; -.
 DR FlyBase; FBgn0005629; nrm.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR002086; Aldenhyde_dehydr.
 DR InterPro; IPR003599; IG-1like.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; IG; 6.
 DR SMART; SM00409; IG; 5.
 DR SMART; SM00408; IGC2; 4.
 DR PROSITE; PS00070; ALDENHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS50835; IG_LIKE; 7.
 KW Immunoglobulin domain.
 SQ SEQUENCE 811 AA; 90442 MW; BAC689EA2C8E23F4 CRC64;
 Query Match 8 9%; Score 117; DB 5; Length 811;
 Best Local Similarity 25.0%; Pred. No. 0.19; Mismatches 30; Gaps 9;
 Matches 48; Conservative 38; Mismatches 76; Indels
 Oy 10 LLLVQLALPAAT-QGNKVLGKGGDTVELTCTASQKSIQFH-----WKNNOI--KIL 62
 Db 26 LVLVLCLALVDSSTAQVDTTISQGESQSVLPCEVDNAEKCKLHSLMMFKDDRIAMTL 85
 Oy 63 GNQGSFLTKGSKLNDRAFSRLMDQGNFPLIKNLKIEDSDTYICEVEDQKEVOLLV 122
 Db 86 GD-----SNVTSYKKEFDERVTV--EQNPYALVIKDKLADIEDYILCDT-----T 128
 Oy 123 FGLTNSDTHLQGSLLTLESPPGSSPSVQCSPPGKNIQGGKITLSVSLQLEIDSGTW 182
 Db 129 FFIIEETCDN-FNGYRIELRLVPP---TEVVIIDAKGRDIKNGSV--VGPMSERQSLKA 182
 Oy 183 TCTVLQNKQKVE 194
 Db 183 TCTYRNRPPQPE 194
 RESULT 83
 Q24273 PRELIMINARY; PRT; 1011 AA.
 AC Q24273;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE NEURONMUSCULIN.
 GN NRM OR CG8779.
 OS *Drosophila melanogaster* (fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94000831; PubMed=8398154;
 RA Kania A., Han P.L., Kim Y.T., Belien H.;
 RT "Neurosecretin, a *Drosophila* gene expressed in peripheral neuronal
 precursors and muscles, encodes a cell adhesion molecule";
 RL Neuron 11:673-687(1993).
 DR EMBL; L23146; AAA03750.1; -.
 DR PIR; T13669; T13669.
 DR FlyBase; FBgn0005629; nrm.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR Pfam; PF00047; IG; 8.
 DR SMART; SM00409; IG; 5.
 DR PROSITE; PS50835; IG_LIKE; 9.
 KW Cell adhesion.
 SQ SEQUENCE 1011 AA; 113125 MW; AFD8A2A015D3AE63 CRC64;

```

Query March      8.9%; Score 117; DB 5; Length 1011;
Best Local Similarity 29.0%; Pred. No. 0.25;
Matches 48; Conservative 38; Mismatches 76; Indels 30; Gaps 9;

QY    10 LLLVLQTALLPAAAT-OGNKVYAGKKDVTVELTCTASOKKSIOFH---WKNNSNOI--KITL 62
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB    26 LVLVLCALAVDSSTAOVDTTITISQGESGVVLPCPVDAEKCGKLSINMFKDDRIAMWL 85

QY    63 GNQGSFUTGSGSKLANDRADRSRLMDGONFLIIKNIKIENDSDTYICGEVEOQKEVVOLL 122
       :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
DB    86 GD-----SNVTSYNKERDERVTN-EQNPRYLVIKDILAIABEDLYLCPT-----T 128

QY    123 FGLTRANSPDHLLQGOSLTFLTESPSSPSVOQSPPREKNIQGGKTSLVSOLIEDSGTW 182
DB    129 FFIEETCDN-FNGRIRIELRVLP--TEVIIIDAKGRIRKNGSV-VGPNQERQSLLKA 182

QY    183 TCTVLOAQKVYE 194
DB    ||||| : : : : 
       183 TCTVRNTRRPOPE 194

RESULT 84
Q7TQ03 PRELIMINARY; PRT; 192 AA.
AC Q7TQ03;
DT 01-OCT-2003 (TREMBLrel.. 25, Created)
DT 01-OCT-2003 (TREMBLrel.. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel.. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CN NCB1 TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blastocyst;
RX MEDLINE=22388257; PubMed=12477932;
RA Klaustner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhut N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.R., Rubin G.W., Hong L.,
RA Stepieton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKewen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M., Buterfield V.S.,
RA Kravynskii M.I., Skalske U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Blastocyst;
RA Strauberg R.;
DR Submitted (May-2003) to the EMBL/GenBank/DBSJ databases.
LR EMBL; BC052651; AAH52651.1; -.
KM Hypothetical protein.
SQ SEQUENCE 192 AA; 20905 MW; EA213FCBE00540D7F CRC64;
```

Oy		69	LTKSPKLNBRADR---	RSIMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEVLVGL	125
Dd		66	WTDO-GHVNRTSRNRYQINSQLLOGNSLTIEAVESDSGLCYCRV-----		111
Oy		126	TANSDTHLLOG----	GSULTLESPPSSPSVOCSPRGKNIIGCKTSLVSQLEIODSGT	181
Dd		112	-----MKGMWDGVQLTTLSLGIOPGSS-----SARTKGIAIG--LSIFPLLVIIVGT		155
Oy		182	WTCVLONOKKVEFKIDIVPRAASALVPAPPGSAL	215	
Dd		156	LVITNYILMKK-----RPPEPSLVAL	176	
 RESULT 85					
ID	O43608	PRELIMINARY;	PRT;	285 AA.	
AC	O43608;				
DT	01-JUN-1998	(TREMBLrel. 06, Created)			
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE	Roundabout 2 (Fragment).				
GN	ROSO2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCHI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98117249; PubMed=9458045;				
RA	Kidd T., Brose K., Mitchell K.J., Feltzer R.D., Tessier-Lavigne M.,				
RA	Goodman C.S., Tear G.,				
RT	"Roundabout controls axon crossing of the CNS midline and defines a				
RL	novel subfamily of evolutionarily conserved guidance receptors.";				
DR	Cell 92:205-215(1998).				
DR	EMBL; AF0400991; AAC39576.1; --				
DR	GO; GO:0008046; F:axon guidance receptor activity; NAS.				
DR	GO; GO:0007417; P:central nervous system development; NAS.				
DR	InterPro; IPR003961; FN_III.				
DR	InterPro; IPR008957; FN_III-like.				
DR	InterPro; IPR003598; IG_c2.				
DR	InterPro; IPR003598; IG_c2.				
DR	Pfam; PF00041; fn3; 1.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SMO0060; FN3; 1.				
DR	SMART; SMO0408; IGC2; 2.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
KM	Immunoglobulin domain.				
FT	NON_TER	1			
FT	NON_TER	1			
SQ	SEQUENCE	285 AA; 285	05DF916A3DBA96C6 CRC64;		
 Query Match 8.8%; Score 116.5; DB 4; Length 285;					
Best Local Similarity 22.8%; Pred. No. 0.053; Indels 69; Gaps 13					
Matches 58; Conservative 32; Mismatches 95;					
Dd		33	KGDYVELICTASOKKSIOGFHKNSNQIKILNGCSFLTKGSKINDRADSRSLMDQNF	92	
Oy		:	: :: :	:	:
Dd		5	QGRVTFFCEJRKNGNPQPAVFQKE-----GSQNLFPNQOQPR---SKCSVPTDD-	53	
Oy		:	: :: :	:	:
Dd		93	PLIIRNKLIKIEDSDTYICEVEDQKEEVLLVG-LTANSD---THLLOGQSILTLESPPG	148	
Oy		:	: :: :	:	:
Dd		54	-LTTINRIORSAGAYICOA-----LTVAGSIILAKOLEVTDVLTTRPPIILIIGGPN	104	
Oy		:	: :: :	:	:
Dd		149	SSPSV-----QC-----RSPRGKNIIGCKTSLVSQLEIODSGT	181	
Oy		:	: :: :	:	:
Dd		105	QTLDVADGTALLKCAATGDPLEVISMLKEGFTFGPHDPA-TIQEGDLQIKRLISTDT	163	
Oy		:	: :: :	:	:
Dd		182	WTCVLONOKKVEFK-IDIVPRA-----SALPAPPGSALPD-----POTASALPD	226	
Oy		:	: :: :	:	:
Dd		164	YTCVAITSSGGASMSAVLDVIESGATISKYNDLSLDPPEPSKPYQVTDVTKNSVTLSMWPG	223	
Oy		:	: :: :	:	:
Dd		227	PPAASALPALAVI	240	

Db 224 TP-CTLPASAVII 235

RESULT 86
Q9V6C2 PRELIMINARY; PRT; 359 AA.
ID Q9V6C2
AC Q9V6C2
DT 01-MAY-2000 (TrEMBLrel. 13 Created)
DT 01-MAY-2000 (TrEMBLrel. 13 Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LAC protein (L033460P).
GN LAC OR CG12369.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132.
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chape M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Bokoy D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Buttle K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibsgen C.,
RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mactel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003822; AAF58506.1; -
DR HSSP; P56276; ITK.
DR FlyBase; FBgn0010238; Lac.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 359 AA; 39939 MW; 12F513E2B9C156F4 CRC64;
Query Match 8.8%; Score 116.5; DB 5; Length 359;
Best Local Similarity 22.3%; Pred. No. 0.072;
Matches 47; Conservative 34; Mismatches 87; Indels 43; Gaps 7;
Db 43 GGTVEPCDSQYAKENVVLFLKTDSDVFLSTGSLTVIKSRFSRLRPDPS-----TYK 97
Qy 94 LIINKLIEDSDTYICE-----VEDQEEVQLVFGLTANSDFLLQGQSITLTLESPPG 148
Db 98 LQIKDIQETDAGTTCQVAVSTVHKVSAEVLSTVRPPVLSID-----NSTQSVASEG 150
Qy 149 SPSVQCRS-----PRGNIGQGTLSVSQLDLQSDSGTWCTVQLON- 189
Db 151 SEVQMECYAGYPTPTITWRNNALIPDSATYVNTLRKIKVKKEDRGTYC-VADNG 209
Qy 190 -----OKVFEKIDIVRASALPAPPGSAL 215
Db 210 VSKCDRNINVEVFAP-VITVPRRLQAL 239

RESULT 87
Q9NCE6 PRELIMINARY; PRT; 570 AA.
ID Q9NCE6
AC Q9NCE6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90299.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Isegai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Maehuo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074780; BAC11205.1; -
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; Ig_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; fn3; 3.
DR Pfam; PF00047; fn3; 3.
DR PRINTS; PR00014; FNTYPELII.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
SQ SEQUENCE 570 AA; 62110 MW; 45CEBDB5B340195 CRC64;
Query Match 8.8%; Score 116.5; DB 4; Length 570;
Best Local Similarity 22.8%; Pred. No. 0.13;
Matches 58; Conservative 32; Mismatches 95; Indels 69; Gaps 13;

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QY 33 KSDTVELTCTASQKSIQFHMKNNSNOIKILGNQGSFLTKGSKLNDRADSRSLMDQGNF 92
DB 48 QGRTVFPFCECTKGNPPQPAVFMQKE-----GSONLLEFPNQPQPN-----SRCSVSPTEGD- 96
QY 93 PLIIKNKIEDSDTYICEVEDQKEVQLVFG-LTANSND---THLLQGQSLTTLTLESPPG 148
DB 97 -LITITNIGRADAGYICQ-----LTVAGSILAAQGLEVTVDLDRPPTIILGGPAN 147
QY 149 SSPSV-----QC-----RSPRGKNIQGGKTLVSQLELQDSGT 181
DB 148 QTLAVDGTALLKCCATGDPPLVISMKEGFTFPGRPDRA-TIOEOGTLQIKNLRIISPTGT 206
QY 182 WTCVTVLQNKQKVERK-IDIVPRA-----SALPAPPTGSALPD---PQTASALPD 226
DB 207 YTCVATSSSGETSKSAVLDTGEGATTISKYDLSDLGFPSPKQVTDVTNKSVTLSWQPG 266
QY 227 PPAASALPALAVI 240
DB 267 TP--GTLPAASAVII 278

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RESULT 88

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Q72681 PRELIMINARY; PRT; 660 AA.
ID 072681
AC 072681
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE Hypothetical protein DKFZp79D0163 (Fragment).
GN DKFZp79D0163.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Mambour R., Heubner D., Mewes H.W., Weill B., Amid C., Oeanger A.,
RA Fodor G., Han M., Wiemann S.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX337757; CAD97826.1; -.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 660 AA; 70374 MW; A6DSBLCSOCBB8815 CRC64;

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Query Match 8.8%; Score 116.5; DB 4; Length 660;
 Best Local Similarity 22.4%; Pred. No. 0.16;
 Matches 52; Conservative 29; Mismatches 76; Indels 75; Gaps 11;

```

QY 27 KVVLGKGGDVELTCTASQKSIQFHMKNNSNOIKILGNQGSFLTKGSKLNDRADSRSL 86
DB 433 KVVASFGQIRMTCTRAEGPPPAIEWQDQ-----PVSSPHQL 473
QY 87 WDQGNPLIIKNKIEDSDTYIC-----EVEDQKEVQLVFG-LTANSPTHLQGSQSLT 140
DB 474 QPDS--LVISRAVEDGGFTYTCVAFNGQDRDQR-WVQLRLGLST-----ISGLPPT 523
QY 141 LTLESPPGSSPSVQC-----RSPRGKNIQGGKTLVSQLELQDSGT 174
DB 524 VTV--PFGDPTARLLCTVAGSIVNIRWSRNGLPVQADGHRVHVSQPDG-----TLTIYNL 574
QY 175 ELQDSGWTCTVLQNKQK-----PFKIDIVPRASALPAPPTGSALPDPTAS 222
DB 575 RARDEGSTCTSAVGSQAVSRSTEVK-VSPAPTPAOPDPERDCVDPPELAN 625

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RESULT 89

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Q865F2 PRELIMINARY; PRT; 739 AA.
ID 0865F2
AC 0865F2
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DE Adhesion molecule VCAM-1.

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GN VCAM-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 1
RP SEQUENCE FROM N.A.
RA Schnurr K., Banning A., Kupper D., Muller-Schmehl K.,
RA Brigelius-Flohe R.;
RT "Modulation of basal and interleukin-1-induced adhesion molecule
RT expression by phospholipid hydroperoxide glutathione peroxidase and
RT 15-lipoxygenase in rabbit aortic smooth muscle cells."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AT212510; AAO52742.1; -.
DB GO; GO:0016020; C:membrane; IEA.
DB GO; GO:0016337; P:cell-cell adhesion; IEA.
DB InterPro; IPR003987; ICAM_VCAM-1.
DB InterPro; IPR003599; IG.
DB InterPro; IPR007110; IG-like.
DB InterPro; IPR003598; IG_c2.
DB InterPro; IPR003989; VCAM-1.
DB Pfam; PF00047; IG_5.
DB PRINTS; PR01472; ICAMVCAM1.
DB SMART; SM00409; IG_5.
DB SMART; SM00408; IGc2_5.
DB PROSITE; PS50835; IG_LIKE; 5.
SQ SEQUENCE 739 AA; 81806 MW; 7AD0D32511E19342 CRC64;

```

Query Match 8.8%; Score 116.5; DB 6; Length 739;
 Best Local Similarity 21.9%; Pred. No. 0.18;
 Matches 50; Conservative 32; Mismatches 69; Indels 77; Gaps 9;

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QY 32 KKGDTVELTCTASQKSIQFHMKNNSNOIKILGNQGSFLTKGSKLNDRADSRSLMDQGN 91
DB 237 QEGSVTMTCSBGLVPEIFW-----SKQDNGNLQRL---SGN 273
QY 92 PLIIKNKIEDSDTYICEVEDO---KEVQLVFGLTANSPTHLQGSQSLTTLTLESPP 147
DB 274 ATLTLAMWEDSGIVCEGVNIGKSRKEVELIV-----QEKPEVEISP 319
QY 148 G-----SSPSVQCSPPRGKNIQGGT-----LSVQLELQDSG 180
DB 320 GPRIAQIDGPVVLTSVAGCETPSFNRTOIDSPANGVTSCTSLTLSVSPRENEH 379
QY 181 TWTCTVLQNKQKVEFKIDI---VPR--ASALPAPPTGSALPDPTAS 222
DB 380 SYLCTVTCGCHKLEKGIQVELYSFPRDPEIELSGPVNGR---PVTVS 424

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RESULT 90

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O95428 PRELIMINARY; PRT; 1235 AA.
ID 095428
AC 095428;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Ratcliffe A.,
RA Madan A., Dickhoff R., Shaffer T., James R., Laeky S., Hood L.;
RT "Complete sequence of the gene for presenilin 1."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL; AF109907; AAC97963.1; -.
DB HSSP; P12111; 2KNT.
DB GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.

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DR InterPro: IPR003598; IG_c2.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR InterPro: IPR000884; TSP1.
 DR Pfam: PF00047; Ig_3.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR Pfam: PF00090; Isp_1; 5.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00408; IGc2; 3.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00209; TSP1; 5.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 DR PROSITE; PS50835; IG_LIKE; 3.
 DR PROSITE; PS50092; TSP1; 5.
 KM Hypothetical protein; Immunoglobulin domain; Protease inhibitor;
 KW Serine protease inhibitor.
 SQ SEQUENCE 1235 AA; 133477 MW; A0B44CE4F3BE350 CRC64;
 Query Match 8.8%; Score 116.5; DB 4; Length 1235;
 Best Local Similarity 22.4%; Pred. No. 0.36; Mismatches 76; Indels 75; Gaps 11;
 Matches 52; Conservative 29; Mismatches 76; Indels 75; Gaps 11;
 QY 27 KVLLEKKGDTVELTCTASQKSIQFHWKNSNQIKILNQGSFLTKGPEKLNDRADSRSL 86
 DB 1008 RVLVDASPGQRIRMTCRAGFPPEPALEMQRDQ-----PVSSPRRQL 1048
 QY 87 WDQGNFLIIKNLKIEDSDTYIC-----EVEDQKEVOLLVFG-ITANSDFHLQGSGLT 140
 DB 1049 QPDGS--LVISRAVDEGDFYTCVAFNGQDRDQ--WVQLRVLGELT-----ISGLPPT 1098
 QY 141 LTLESPPGSSPSVOC-----RSPRGKNIQSGKTLVSQSL 174
 DB 1099 VTV--PEEDTARLLCVVAGESVNIWNSKNGLPVQADGRVHVSPPG-----TLLIYNL 1149
 QY 175 ELQDSGTWTCTVLQNKQKTV---EFKIDIVPRASALPAPPGSALPDQTS 222
 DB 1150 RAPDGSYTCGAYQGSQAVNSSTEVK-VSPAFTAQPRDPCGDCQDELAN 1200
 RESULT 91
 Q9HCK4 PRELIMINARY; PRT; 1380 AA.
 AC Q9HCK4:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA1568 (Fragment).
 GN KIAA1568.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20450683; PubMed=10997877;
 RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.
 RT XVIII. The complete sequences of 100 new cDNA clones from brain which
 RT code for large proteins in vitro.";
 RL DNA Res. 7:273-281(2000).
 DR EMBL; AB046788; BABJ3394.1; -.
 DR HSSP; P56276; ITK.
 DR Genew; HGNC:10250; ROBO2.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00041; fn3; 3.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00060; FN3; 3.
 DR SMART; SM00408; IGc2; 5.
 DR PROSITE; PS50835; IG_LIKE; 5.

KM Hypothetical protein; Immunoglobulin domain.
 FT NON TER 1 151426 MW; 45BE63B2EFA26732 CRC64;
 SQ SEQUENCE 1380 AA; 151426 MW; 45BE63B2EFA26732 CRC64;
 Query Match 8.8%; Score 116.5; DB 4; Length 1380;
 Best Local Similarity 22.8%; Pred. No. 0.42;
 Matches 58; Conservative 32; Mismatches 95; Indels 69; Gaps 13;
 QY 33 KGDVELTCTASQKSIQFHWKNSNQIKILNQGSFLTKGPEKLNDRADSRSLMDQNF 92
 DB 329 QGRTVTPPCETKGNPPAPVFWQKE-----GSQNLPEPNQPN-----SCSVSPTD- 377
 QY 93 PLIKNLKIEDSDTYICEVEDQKEVOLLVFG-ITANSDFHLQGSFLTKGPEKLNDRADSRSLMDQNF 148
 DB 378 -LITNIOKSPAGYITCA-----LTVAGSLAKAQLEVTVDLDRPPPIILQGAN 428
 QY 149 SSPSV-----QC-----RSPRGKNIQSGKTLVSQLELQDSGT 181
 DB 429 QTLAVDGTALCKATGDPFLVISMKEGFTFPPDPDRA-TIQCGTLQINLRISPTGT 487
 QY 182 WTCVTLQNKQKVER--IDIVPRA-----SALPAPPGSALPD---POTASALPD 226
 DB 488 YTCVATSSSGETSSAVLDVTGSGATISKYDLSLDLPQPPKPVTVTKNSVTLSQPG 547
 QY 227 PPAASALPALAVI 240
 DB 548 TP--GTLPAAYII 559
 RESULT 92
 Q8NAO3 PRELIMINARY; PRT; 354 AA.
 AC Q8NAO3:
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ34988.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Salto K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Magatsuna M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
 RT "NDO human cDNA sequencing project.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK092307; BAC03858.1; -.
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGc2; 3.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KM Hypothetical protein; Immunoglobulin domain.
 KW Serine protease inhibitor.
 SQ SEQUENCE 354 AA; 38779 MW; 5DC938094E35964A CRC64;
 Query Match 8.8%; Score 116; DB 4; Length 354;
 Best Local Similarity 22.6%; Pred. No. 0.078;
 Matches 52; Conservative 36; Mismatches 94; Indels 48; Gaps 10;
 QY 20 PAATQGNKVLVIGKKGDTVELTCTASQKSIQFHWKNSNQIKILNQGSFLTKGP-----SK 75
 DB 41 PMAAVDMMV--RKGDPAVLRCTYLEDGAS--KGALNRSIIIFAG--GDKNSVDPRAVIST 95
 QY 76 LNDRADSRSLMDQNFPLIIKNLKIEDSDTYICEVEDQKEVOLLVFGTLA----- 127

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Db      96 LNKR-----DYSLOQVNDVDDGPYTSVOTQTPRTMOYH-LTVQVPPKIYD 143
Qy      128 -NSDTHLLOQOSLTLTLESPPGSSPVQCR--SPRGKNIQGGKTLVSQLELQDSTWTC 184
Db      144 ISNDMTVEGNTVLTCLATGKPEPFISWHISPSAPFNQGLDIYGTTRQAGYEYC 203
Qy      185 TV-----LQNKVKEFKIDIVPRASALPAPT-----GSLALPD 218
Db      204 SAENDVSFPDVRKVVNPAFTIQEIKSGTVTPGRSGLIRCEGAVPPP 253

RESULT 93
Q991A6 PRELIMINARY; PRT; 484 AA.
AC Q991A6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003495; AA03495.1; -.
DR PIR; F33932; F33932.
DR HSSP; P01810; 2RBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03006; Ig_MHC.
DR InterPro; IPR03596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KM Hypothetical protein.
SQ SEQUENCE 484 AA; 52567 MW; 8BEA4F9BCF582PA CRC64;

Query Match 8.8%; Score 115.5; DB 11; Length 484;
Best Local Similarity 23.3%; Pred. No. 0.13;
Matches 70; Conservative 32; Mismatches 117; Indels 81; Gaps 12;

Qy      13 VLQALIPAAATQGNKV-----VLGKGDVLELTCTASQKKSIGF--HMKNNOIKI 61
Db      4 VWTLLFLPMAAQAQSIQAIQIVQSGPELKKPGEIVKISCKASGYFTDYSMHWVQAQPKG 63
Qy      62 LGNGGSF-LRTGPKKLNDRADSRSL---WDQGFPLIKLKIEDSDTYICEVEDQKEE 117
Db      64 LKMWGWNIEGESVADDFKGRPAFSLFTSASTIHLQINNLKNEIDATATYFCARSDYD 123
Qy      118 VOLLVFGLTANSDFHLQOSLTLTLES-----PPGSS-----PS 152
Db      124 IYAM-----DYMQGGSIVTVSSSARNPITYPLTLPPALSSDVIIIGCLIHDFPS 174
Qy      153 VQCRSPRGKN-----IQGKTLVSQLELQDSTWTCVLQNKVKE 194
Db      175 GTMNVTVGKSGKDIITVNFPPALASGRYTWSSQLTPAVECPGEGSVKCSVQHDSPVQ 234
Qy      195 FKIDIVPRASALPAPPGSALPDPTQTSALPDPPRASAALPALAVIFLLGLGIVACVL 254
Db      235 -ELDV---NCSGPTPPPTITPSCQPSLSLQRP-----ALEDLLGSDASTICTL 280

RESULT 94
Q97PD3 PRELIMINARY; PRT; 820 AA.
AC Q97PD3;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

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DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055333; AAH55333.1; -.
KM Hypothetical protein.
SQ SEQUENCE 820 AA; 90951 MW; ECB1FD26983065E CRC64;

Query Match 8.8%; Score 115.5; DB 11; Length 820;
Best Local Similarity 23.6%; Pred. No. 0.26;
Matches 60; Conservative 28; Mismatches 97; Indels 69; Gaps 13;

Qy      33 KQDTELTCTASQKKSIGFHMKNNOIKILGNGGSFVLTGPKSLNDRADSRRLMDQGNF 92
Db      331 QGRTVFPCEITKPNPPAVFWQK-----GSONLLFPNQPOQPN---SRCSVSTGID- 379
Qy      93 PLIRKLIKIEDSDTYICEVEDQKEEVQLVFG-----LTANSDFHLQOS--- 136
Db      380 -LITNIGRSDAGYICQA-----LVAGSIILAKQLEVTDLVTRDPPITLLOPIN 430
Qy      137 QSL-----TLTLESPGSSP-----SVQCRSPRGKNIQGGKTLVSQLELQDST 181
Db      431 QTLAVDGTALLKCKATGEBPLPVISLKEGFTFLGRPPRA-TIQQDQTLQIKNLRIDTGT 489
Qy      182 WTCVTVLQNKVKEFK--IDIVPRASA-----LPAPPGSALPDQ---TASALPD 226
Db      490 YTCVAVTSSSGEFTSMAVLDTESGATISKYVDMNDLPGEPSKQVTVDSKNSVTLQWPG 549
Qy      227 PPAASALPALAVI 240
Db      550 TP--GVLPASAVYII 561

RESULT 95
Q9VY33 PRELIMINARY; PRT; 344 AA.
AC Q9VY33; Q95SR2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE CG32600 protein (GH05565p).
GN CG32600 OR CG5291 OR CG14477 OR CG14445.
OS Drosophila melanogaster (Fruit fly).

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RA Klauener R.D., Collins F.S., Wagner L., Shennan C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan R.F., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Dapkin L., Maruoka K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
 RA Krzywnski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005332; AAI05332.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25702 MW; 7FBPE4ED23084BC6 CRC64;
 Query Match 8.7%; Score 114.5; DB 4; Length 236;
 Best Local Similarity 28.6%; Pred. No. 0.062;
 Matches 57; Conservative 20; Mismatches 77; Indels 45; Gaps 10;
 QY 11 LVLVQLALPAA-----TGKRVYLGKGDVYELTCTASQKSIQFMKNSNQIKLGN 64
 DB 9 LLLGLLFCFGARCDIQTPSSLSASVSDVTYITCRASQDISNYLAWFOQKP---GK 64
 QY 65 QGSFLLTKGPKLNDRAISRSLMDQG-NPFLIKIKLIEDSDPYICEVEDQKEEVQLLV 123
 DB 65 APTSLLTGASLSQSGVSKSGSGSDFTLITLSSLDPEPATYTC---QQRKSYVTF 120
 QY 124 GLTANSDTHLLQGSLTLTLSPGSSPSVQCRSPKKNIGGKTLSSVSLQLDQSGTWT 183
 DB 121 G-----GQTKLEI---KRTVAAPSVFIFPPSDEQKLSG-TASV-----V 155
 QY 184 CTVLQN---QKRYEFKID 198
 DB 156 C-LINNFYPREAKVQMKVD 173
 RESULT 97
 Q8UUG3 PRELIMINARY; PRT; 308 AA.
 AC Q8UUG3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Novel immune-type receptor 2.
 GN NTR2.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OC NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21574523; PubMed=11698645;
 RA Hawke N.A., Yoder J.A., Haire R.N., Mueller M.G., Litman R.T.,
 RA Miracle A.L., Stuge T., Shen L., Miller N., Litman G.W.,
 RT "Extraordinary variation in a diversified family of immune-type
 RT receptor genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:13832-13837(2001).
 DR EMBL: AF397467; AAL35555.1; -
 DR EMBL: AF397455; AAL35543.1; -

DR GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00409; IG_2.
 DR PROSITE: PS00835; IG-LIKE; 2.
 KW Receptor.
 SQ SEQUENCE 308 AA; 34259 MW; A1AD3192157A572 CRC64;
 Query Match 8.7%; Score 114.5; DB 13; Length 308;
 Best Local Similarity 21.7%; Pred. No. 0.088;
 Matches 55; Conservative 35; Mismatches 88; Indels 75; Gaps 11;
 QY 10 LLLVQLALPAA-----GKRVYLGKGDVYELTCTASQKSIQFMKNSN---QIKIG 63
 DB 7 LLLCEPLHLVKTQTPRNSDSLVPFAEGSVNISCIYESDMVHMFYKYNIGQKPKLS 66
 QY 64 NGQSFLLTKGPKLNDRAISRSLMDQG-NPFLIKIKLIEDSDPYICEVEDQKEEVQLLV 122
 DB 67 NFYKYDKKATFHHEPKNARFPMVNEKSKTNLEIKQLQSDSATYTC---GSANINYE 122
 QY 123 FG---LTANSDTHLLQGSLTLTLSP-----PGSSPSVOC-----R 156
 DB 123 FGSGETLVVQASQHSLS-----VLQQPVHELHPGGSYTLHCTVITDRCAGEHSYVPR 176
 QY 157 SRPG-----KNIQGK-----TLSVQLDQSGTWTCTV----- 186
 DB 177 HNSGSHPGVITYTHGDSNGRCCKNPAGSLTMCVYSLPKTNLSTSDVGTYHCAVAACQ 236
 QY 187 --LQNKVYEFKI 197
 DB 237 ILFGNTKIDMKI 249
 RESULT 98
 Q96SC3 PRELIMINARY; PRT; 2673 AA.
 AC Q96SC3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Fibulin-6 (Fragment).
 GN FIBL-6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RA Kostka G., Timpi R.,
 RT "Partial sequence of fibulin-6 with a C-terminal region related to
 RT domain II and III of the fibulin family";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ306906; CAC37630.1; -
 DR GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR00152; Asx_hydroxyl_S.
 DR InterPro: IPR00875; Cecropin.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR009017; GFP-like.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003598; IG_C2.
 DR InterPro: IPR00884; TSP1.
 DR InterPro: IPR008085; TSP_1.
 DR Pfam: PF00008; EGF_5.
 DR Pfam: PF00047; IG_17.
 DR Pfam: PF00090; TSP_1; 6.
 DR PRINTS: PR01705; TSP1REPEAT.
 DR SMART: SM00179; EGF_CA; 7.
 DR SMART: SM00408; IG_C2; 17.
 DR SMART: SM00209; TSP1; 6.
 DR PROSITE: PS0010; ASX_HYDROXYL; 5.

DR PROSITE; PS00268; CECROPIN; 1.
 DR PROSITE; PS01186; EGF 2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 DR PROSITE; PS50835; IG_LIKE; 17.
 DR PROSITE; PS50092; TSP1; 6.
 KM EGF-like domain; Immunoglobulin domain.
 FT NON TER
 SQ SEQUENCE 2673 AA; 291017 MW; BEAEC30B8340E272 CRC64;

Query Match 8.7%; Score 114.5; DB 4; Length 2673;
 Best Local Similarity 20.9%; Pred. No. 1.5;
 Matches 66; Conservative 40; Mismatches 93; Indels 117; Gaps 13;

QY 1 MNRGVPRHLLVQLLPPAATGKGVKGGDTVELTCTASQKSIOPHMKN----- 55
 DB 415 LKNDLP---LPLSHIRLL-NAAGVIRIVRAQVSDVAVYTCVASNRAGVNDKHYNLQVFA 470
 QY 56 -SNOIKILGNQSGFLTKGPKS---LNDRADSRSLMDQGNPL-----IIK 97
 DB 471 PRMNDNMGTREIIVLKGSSITSMACITDGTAPAMARDQPIGLDHLTVSTHGMVLQ 530
 QY 98 NLK--IEDSTYIC-----EV-----EDQKEEVOLLV----- 122
 DB 531 LLKAEIEDSGKYTCIASNEAGEVSKHFLKYLEPPHNGSEHEIEIVVNNPLELTGIA 590
 QY 123 FGLTANSDTHLQOQSLLTLIESPPGSSPVQCRSPKKNIOGKKTLSVQLDELQDSGTW 182
 DB 591 SGIDPAPKMTWKDGRPLPQT-----DQVITGGGEVARISTAQVEDGTRY 635
 QY 183 TC-----TVLON--OKYVEFKIDIVPRASALPAP 209
 DB 636 TCLASSPAGDDKREYLVKRVHPNIACTDEPRDITVLNRQVTECKSDAVP-----P 688
 QY 210 PTGSALPDPOGTASALP 225
 DB 689 PVITWLNNGERLQATP 704

RESULT 99

Q723W6 PRELIMINARY; PRT; 338 AA.
 AC Q723W6;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein DKFZp686H1949.
 GN DKFZp686H1949.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Human amygdala;
 RA Wamburt R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX537377; CAD97619.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 338 AA; 37267 MW; EDD86BE2C57809E3 CRC64;

Query Match 8.7%; Score 114; DB 4; Length 338;
 Best Local Similarity 23.0%; Pred. No. 0.11;
 Matches 59; Conservative 41; Mismatches 101; Indels 56; Gaps 11;
 QY 4 GVPFRHLLVQLLPPAATGKGVKGGDTVELTCTASQKSIOPHMKNSNOIKILG 63
 DB 21 GVPFRS-----GDATFPKAMDN---VTVQGESATLRTITDRYT-RVAMLNRSITLYAG 71
 QY 64 N-----QGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEV----- 112
 DB 72 NDKMSIDBRVILVNTFTQ-----YSIMIQNVADVDEGPTGCVQTDNH 115

QY 113 DQKEVOLLVFG---LTANSDTHLQOQSLLTLIESPPGSSPVQCRSPKKNIOG--- 165
 DB 116 PKTSRHLIVQVPRQIMNISSDITVNEGSSVTLICLAGRPETVTRHLSVNEGQFVS 175
 QY 166 -GKTLVSQLELDGSGTWCTVLO----NOKYVEFKIDIVPRASALPAPPTGSALPDPO 219
 DB 176 EDEYLFIISDIKIQSGEYECSSALNDVAAPVRKVIIVNPPYIS--KAKNTGVSQOKG 233
 QY 220 TASALPDPPASALPAP 236
 DB 234 ILSC-----BASAVPMA 245

RESULT 100

Q8N3J6 PRELIMINARY; PRT; 435 AA.
 AC Q8N3J6;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZP761G128.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Amalgala;
 RA Koehler K., Beyer A., Mewes H.W., Well B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL034270; CAD38945.1; -
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGC2; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 435 AA; 47554 MW; 59DD41B7F34D446 CRC64;

Query Match 8.7%; Score 114; DB 4; Length 435;
 Best Local Similarity 21.6%; Pred. No. 0.15; Mismatches 88; Indels 82; Gaps 13;
 Matches 58; Conservative 40; Mismatches 88; Indels 82; Gaps 13;
 QY 33 KGDVPELTC-TASQKSIOPHM-KNSNOIKIL-----GNQGSFLTKGPKSLNDRADSR 83
 DB 138 EGDLMQTLCTGSGSKPAADIRMFNDKEIKDVKYLKEEDANRKTFVS--STLDFRVD-- 193
 QY 84 RSLMDQGNFPLIKNLKIEDSDTYICEVEDQK---EVQLLVFGLTANSDTHL----- 134
 DB 194 -----RSDGVAVICRVHDHESLNATPQVAMQVLEIHYTPSVKLIPTPF 237
 QY 135 --QGOSLTLIESPPGSSPVQCRSPG-----KNIGKKTLSVQLDELQDSGTWC- 184
 DB 238 PQSGPFLITCESGKFLPEVATMTKDGGLPDPDRNVVSGRELNIPLNKTNDGTYRCE 297
 QY 185 -TVLONOKYVEFKI-----DIVPRAS-----ALPAPPTGSALPDPOGTASA 223
 DB 298 AFTNTIGSSASAEVLIIVDVENTLLPTIIPSLTATVTTVAITTSPTTSA-----TTSS 352
 QY 224 LPDP-----PAASALPALAVISFL 243
 DB 353 IDPNALAGONGPDHALIGIVAVVVFV 380

Search completed: August 3, 2004, 13:13:40
 Job time : 22.7158 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 12:50:09 ; Search time 26.2483 Seconds
(without alignments)
2777.216 Million cell updates/sec

Title: SEQ6
Perfect score: 1317
Sequence: 1 MNRGVPRHLLVLQLALP.....VISFLGLGVACVLARR 258

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 125 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041.5	79.1	449	6	AAE37576 Human FDI
2	1038	78.8	310	2	AAE26784 CD4-IgG2
3	1038	78.8	310	2	AAE46680 CD4-Kappa
4	1038	78.8	310	3	AAE85081 CD4-Kappa
5	1038	78.8	310	4	AAE67324 CD4-Kappa
6	1038	78.8	310	4	AAE80885 Human CD4
7	1038	78.8	310	6	ABG71124 CD4-Kappa
8	1036.5	78.7	450	6	AAE37574 Human DID
9	1033	78.4	534	2	AAE26531 Sequence
10	1032.5	78.4	432	2	AAE26782 CD4-gamma
11	1032.5	78.4	432	2	AAE46678 CD4-gamma
12	1032.5	78.4	432	3	AAE85079 Human CD4
13	1032.5	78.4	432	4	AAE67322 CD4-gamma
14	1032.5	78.4	432	4	AAE80883 Human CD4
15	1032.5	78.4	432	6	ABG71122 CD4-gamma
16	1030.5	78.2	530	2	AAE26783 CD4-IgG2
17	1030.5	78.2	530	3	AAE85080 CD4-IgG2
18	1030.5	78.2	530	4	AAE67323 CD4-IgG2
19	1030.5	78.2	530	6	AAE80884 Human CD4
20	1030.5	78.2	530	6	ABG71123 CD4-immun
21	1029	78.1	203	2	AAE78674 CD4 domain
22	1029	78.1	203	2	AAE89451 CD4-D1-D2
23	1029	78.1	398	2	AAE78673 CD4 domain
24	1029	78.1	398	2	AAE89450 CD4-D1-D4
25	1029	78.1	400	2	AAE06374 Truncated

26	1029	78.1	402	1	AAE91922 Sequence
27	1029	78.1	402	1	AAE94757 Sequence
28	1029	78.1	458	1	AAE91990 Clone pT4
29	1029	78.1	458	1	AAE91369 T4 protei
30	1029	78.1	458	2	AAE13491 Human CD4
31	1029	78.1	458	2	AAE939826 Soluble h
32	1029	78.1	458	3	AAE80769 DNA encod
33	1029	78.1	462	2	AAE27277 CD4:eta p
34	1029	78.1	462	2	AAE78677 T-cell re
35	1029	78.1	462	2	AAE89457 CD4:gamma
36	1029	78.1	462	2	AAE02214 CD4:Fc re
37	1029	78.1	462	2	AAE83142 ChimERIC
38	1029	78.1	532	2	AAE27278 CD4:gamma
39	1029	78.1	532	2	AAE78678 T-cell re
40	1029	78.1	532	2	AAE89458 CD4:eta f
41	1029	78.1	532	2	AAE02215 CD4:T-cel
42	1029	78.1	532	2	AAE83141 ChimERIC
43	1029	78.1	532	2	AAE27276 CD4:zeta
44	1029	78.1	532	2	AAE78676 T-cell re
45	1029	78.1	532	2	AAE89456 CD4:zeta
46	1029	78.1	532	2	AAE02213 CD4:T-cel
47	1029	78.1	532	2	AAE83140 ChimERIC
48	1029	78.1	2037	2	AAE04032 Full leng
49	1029	78.1	2030	2	AAE07641 Deduced s
50	1027	78.0	310	2	AAE26532 Sequence
51	1026.5	77.9	530	2	AAE46679 CD4-IgG2
52	1026	77.9	394	1	AAE93506 Derived s
53	1023	77.7	202	6	AAE37197 sCD4 prot
54	1023	77.7	295	2	AAE07605 Plasmid T
55	1023	77.7	318	2	AAE07606 Plasmid T
56	1023	77.7	394	2	AAE939825 Soluble h
57	1023	77.7	394	2	AAE88328 T4 glycop
58	1023	77.7	416	3	AAE19509 CD4-IgM f
59	1023	77.7	436	3	AAE51080 Human fus
60	1023	77.7	458	3	AAE88329 T4 glycop
61	1023	77.7	458	4	AAE81502 Human CD4
62	1023	77.7	458	4	AAE79087 Amino ac
63	1023	77.7	458	7	ADD25609 Binding d
64	1023	77.7	458	7	ADBE57489 Human Bro
65	1023	77.7	473	7	ADA44807 CD4/TCR C
66	1023	77.7	474	3	AAE59170 CD4-Ig fu
67	1023	77.7	481	3	AAE19510 CD4-IgM f
68	1023	77.7	481	3	AAE59171 Human fus
69	1023	77.7	481	3	AAE59171 CD4-Ig fu
70	1023	77.7	507	3	AAE80158 sCD4-SCFV
71	1023	77.7	519	2	AAE20152 Human CD4
72	1023	77.7	616	3	AAE51082 Human fus
73	1023	77.7	631	1	AAE93009 Genetic c
74	1023	77.7	631	3	AAE19508 CD4-IgG1
75	1023	77.7	631	3	AAE51079 Human fus
76	1023	77.7	631	3	AAE59169 CD4-Ig fu
77	1023	77.7	729	1	AAE93008 Genetic c
78	1023	77.7	729	3	AAE19507 CD4-IgG1
79	1023	77.7	729	3	AAE51078 Human fus
80	1023	77.7	729	3	AAE59168 CD4-Ig fu
81	1023	77.6	435	2	AAE26530 Sequence
82	1021.5	77.6	435	7	ADBE5841 Human CD4
83	1021	77.5	614	1	AAE93012 Genetic c
84	1018	77.3	481	1	AAE30011 Genetic c
85	1015	76.8	394	3	AAE80768 The solub
86	1012	76.8	394	3	AAE6377 T4 encode
87	1009	76.6	458	2	AAE94703 Sequence
88	1009	76.6	524	1	AAE07640 Deduced p
89	1009	76.6	2458	2	AAE04031 Full leng
90	1009	76.6	2458	2	AAE04910 T4 protei
91	1004	76.2	458	2	AAE11285 gp120 bin
92	1002	76.1	458	2	AAE20151 Chimpanze
93	999	75.9	458	2	AAE10988 Chimpanze
94	999	75.9	458	2	AAE20150 Chimpanze
95	994	75.5	400	1	AAE93010 Genetic c
96	982	74.6	616	3	AAE19511 CD4-IgG1
97	969	73.6	400	2	AAE0154 Sol. rhos
98	954	72.4	400	2	

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99 946 71.8 458 2 AAR15149 Aar15149 CD4 coord
100 916 69.6 384 1 AAP90833 Aap90833 Amino aci
101 916 69.6 434 1 AAP96151 Aap96151 Sequence
102 916 69.6 434 1 AAP93557 Aap93557 Fusion of
103 916 69.6 729 2 AAR41042 Aar41042 CD4-GRPH
104 916 69.6 942 2 AAR41041 Aar41041 CD4-GSP13
105 916 69.6 1786 2 AAR41043 Aar41043 CD4-SBA17
106 914 69.4 410 2 AAW35860 Aaw35860 Human CD4
107 912 69.2 458 2 AAR20148 Aar20148 Cynomolgus
108 910 69.1 400 2 AAR20149 Aar20149 Sol. rhcs
109 909 69.0 458 2 AAR10987 Aar10987 Rhesus mo
110 905 68.7 375 2 AAR07721 Aar07721 Recombina
111 903 68.6 333 2 AAR04926 Aar04926 Immunopro
112 903 68.6 435 2 AAP90992 Aap90992 Human CD4
113 901.5 68.5 549 2 AAR04920 Aar04920 Immunopro
114 901.5 68.5 557 2 AAR04923 Aar04923 Immunopro
115 899 68.3 178 6 ABU07701 Abu07701 Viral coa
116 899 68.3 185 2 AAY14206 Aay14206 HIV-1 gp1
117 899 68.3 195 2 AAY14210 Aay14210 HIV gp120
118 899 68.3 217 2 AAR15150 Aar15150 PCDA-gels
119 899 68.3 369 2 AAY39824 Aay39824 Soluble h
120 899 68.3 369 3 AAY68327 Aay68327 T4 glycop
121 899 68.3 370 1 AAP93528 Aap93528 Human sol
122 899 68.3 370 4 AAB83356 Aab83356 Human CD4
123 899 68.3 433 3 AAY54500 Aay54500 Amino aci
124 899 68.3 530 6 ABU07697 Abu07697 Viral coa
125 899 68.3 720 6 ABU07694 Abu07694 Viral coa

```

ALIGNMENTS

RESULT 1

AAE37576 standard; protein: 449 AA.

ID AAE37576;

DT 27-AUG-2003 (first entry)

XX Human FDIID2-Ig alphatp fusion protein variant.

XX Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;

XX human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; DI;

XX DI; alpha tailpiece; alphatp; fusion protein; mutcin; variant; mutant.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Misc-difference 218 /note= "Wild type Glu substituted with Pro"

XX FT Misc-difference 219 /note= "Wild type Leu substituted with Val"

XX FT Misc-difference 221 /note= "Wild type Gly substituted with Ala"

XX MO2003040311-A2.

XX 15-MAY-2003.

XX 24-OCT-2002; 2002WC-US034393.

XX 25-OCT-2001; 2001US-0346231P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Arthos J, Cicala C, Fauci AS;

XX WPI; 2003-441545/41.

XX N-PSDB; ACG82877.

XX New CD4 polypeptide ligated at its C-terminus with a portion of an

XX immunoglobulin, useful for preparing a composition for treating or

PT preventing HIV-1 infection.

XX Example 11; Page 67; 100pp; English.

XX The invention relates to a CD4 (cluster of differentiation factor 4)

XX polypeptide ligated at its C-terminus with a portion of an immunoglobulin

XX (Ig) comprising a hinge region and a constant domain of a mammalian Ig

XX heavy chain. The polypeptide comprises a tailpiece from the C-terminus of

XX the heavy chain of an IgA or IgM antibody. Polypeptides of the invention

XX are useful for preparing a composition for treating or preventing human

XX immunodeficiency virus (HIV)-1 infection. The invention is useful in gene

XX therapy and also in the preparation of vaccines. The present sequence is

XX a fusion protein variant (G218P/L219V/220delA/G221A) which comprises a

XX human IgA alpha tailpiece (alphatp), a human IgG2 constant region

XX comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain.

XX This variant protein is also referred to as mutant F

XX Sequence 449 AA;

SQ Query Match 79.1%; Score 1041.5; DB 6; Length 449;

Best Local Similarity 85.4%; Pred. No. 2.4e-64;

Matches 210; Conservative 6; Mismatches 17; Indels 13; Gaps 3;

QY 1 NMRGVPFRHLIVLQALIPAAATQGNKYLGKKDVEITCTASQKSIQFMKNSNQIK 60

DB 1 NMRGVPFRHLIVLQALIPAAATQGNKYLGKKDVEITCTASQKSIQFMKNSNQIK 60

QY 61 ILGNQSFLLTKGSPSLNDRADSRSLMDQGNPPLIKIKIDSDTYICEVDQKEEYOL 120

DB 61 ILGNQSFLLTKGSPSLNDRADSRSLMDQGNPPLIKIKIDSDTYICEVDQKEEYOL 120

QY 121 LVFGLTANSDFHLLQGOSLITLTESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

DB 121 LVFGLTANSDFHLLQGOSLITLTESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

QY 181 TWCTVLOKQKVERKIDIVPPASA-----LAPP-TGSAL----PDPTASALPMP 227

DB 181 TWCTVLOKQKVERKIDIVPPASA-----LAPP-TGSAL----PDPTASALPMP 227

QY 228 PAASAL 233

DB 241 PEVTCV 246

QY 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

DB 241 PEVTCV 246

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XX 08-FEB-1991; 91US-00653684.
PR (PROG-) PROGENICS PHARM INC.
XX Beauty GA, Maddon PJ;
XX WPI; 1992-300034/36.
XX DR N-PSDB; AAQ28090.
XX CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
XX PT treatment, prevention and diagnosis of HIV infection.
XX PS Claim 16; Fig 5; 90pp; English.
XX
XX This sequence represents a CD4-IgG2 chimeric heavy chain heterotrimer
XX it was produced by expression of the coding mutagenised cDNA (produced as
XX described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently
XX assembled intracellularly and effectively secreted from mammalian cells
XX pref. CHO, COS, or myeloma cells as a heterotrimer, enabling high
XX recovery and purification from the medium of cells expressing it. It
XX possesses increased serum half-life and has increased avidity for HIV cf.
XX heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block
XX the spread of HIV infection within a patient. Attachment to a detectable
XX marker makes it useful in an assay for HIV or SIV infection, and it can
XX also be linked to toxins, eg diphtheria, Pseudomonas exotoxin A (domains
XX I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003
XX to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 310 AA;
XX
XX Query Match 78.8%; Score 1038; DB 2; Length 310;
XX Best Local Similarity 85.7%; Pred. No. 2.8e-64;
XX Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;
XX
XX 1 MNRGVFRRHLLVQLALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
XX Db 1 MNRGVFRRHLLVQLALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
XX
XX 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
XX Db 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
XX
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX Qy 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX
XX 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPAPASALPALAVI 240
XX Db 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPAPASALPALAVI 240
XX
XX 241 SFLL 244
XX Qy 241 SFLL 244
XX
XX 229 VCCL 232
XX Db 229 VCCL 232
XX
XX RESULT 3
XX AA46680 standard; protein; 310 AA.
XX
XX AA46680;
XX
XX 25-MAR-2003 (revised)
XX DT 08-AUG-1994 (first entry)
XX
XX CD4-kappa light chain.
XX
XX CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV;
XX human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
XX imaging; detection; targeting; immunoglobulin; IgG.
XX
XX Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Region 1..204
FT /label= CD4 Region.
FT Region 205..310
FT /label= Kappa Region.
XX
XX MO9403191-AL.
XX
XX 17-FEB-1994.
XX
XX 06-AUG-1993; 93WO-US007422.
XX PF
XX 07-AUG-1992; 92US-00927931.
XX PR
XX (PROG-) PROGENICS PHARM INC.
XX
XX Allaway GP, Maddon PJ;
XX PI
XX WPI; 1994-065392/08.
XX DR N-PSDB; AAQ57752.
XX
XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
XX PT immunoconjugates - used to kill HIV-infected cells and to image and
XX stage HIV infection.
XX
XX Disclosure; Fig 5; 142pp; English.
XX
XX A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy
XX chains (AA46679) and two kappa light chains or CD4-kappa light chains is
XX linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide
XX of low to moderate cytotoxicity. The resulting immunoconjugate comprising
XX the toxin can be used to kill HIV infected cells and to treat HIV
XX infected subjects to reduce the population of HIV infected cells. It can
XX also be used to reduce the likelihood of infection. The immunoconjugate
XX comprising the radionuclide can be used to image HIV infected tissue, to
XX calculate the stage of HIV infection or the efficacy of an anti-HIV
XX treatment using the imaging technique and for determining the prognosis
XX of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 310 AA;
XX
XX Query Match 78.8%; Score 1038; DB 2; Length 310;
XX Best Local Similarity 85.7%; Pred. No. 2.8e-64;
XX Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;
XX
XX 1 MNRGVFRRHLLVQLALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
XX Db 1 MNRGVFRRHLLVQLALIPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
XX
XX 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
XX Qy 61 ILGNQGSFLTKGSPSKUNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
XX
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX Db 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
XX
XX 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPAPASALPALAVI 240
XX Qy 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPPAPASALPALAVI 240
XX
XX 241 SFLL 244
XX Db 241 SFLL 244
XX
XX 229 VCCL 232
XX Qy 229 VCCL 232
XX
XX RESULT 4
XX AA485081
XX ID AA485081 standard; protein; 310 AA.
XX
XX AA485081;
XX
XX 19-JUN-2000 (first entry)
XX

```

```

XX CD4-kappa chimeric light chain amino acid sequence.
DE
XX
KM CD4-kappa chimeric light chain; immunoglobulin; treatment: CD4-IgG2;
KW cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW cellular immune response interaction mediator; HIV interaction; staging;
KM prognosis; envelope glycoprotein burden; human.
XX
OS Homo sapiens.
PN US6034223-A.
XX
PD 07-MAR-2000.
XX
PF 07-JUN-1995; 95US-00477460.
XX
PR 07-AUG-1992; 92US-00927931.
PR 06-AUG-1993; 93WO-US007422.
PR 03-FEB-1995; 95US-00379516.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
PI Allway GP, Maddon PJ;
XX
DR MPI; 2000-269502/23.
XX
DR N-PSDB; AA298857.
XX
PT New immunoglobulin, used to treat, prevent or image human immune
PT deficiency virus infection, comprises radionuclide attached to
PT heterotetramer of CD4-immunoglobulin chimeras.
XX
PS Disclosure; Fig 5; 58pp; English.
XX
CC This sequence represents the CD4-kappa chimeric light chain amino acid
CC sequence of the CD4-IgG2 chimeric heterotetramer. The invention relates
CC to an immunoglobulin comprising a cytotoxic radionuclide and a
CC heterotetramer of two heavy chains and two light chains. The cytotoxic
CC radionuclide is linked to either the heavy chains or the light chains, or
CC to all four chains, directly or through a bifunctional chelator. Both
CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
CC vector CD4-IgG2HC-PRCMV (ATCC 75193) and both light chains are chimeric
CC CD4-kappa chains encoded by vector CD4-KLC-PRCMV (ATCC 75194). CD4 is a
CC non-polymorphic cell surface glycoprotein that is expressed on the
CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC and dendritic cells. CD4 associates with major histocompatibility complex
CC (MHC) class II molecules on the surface of antigen presenting cells to
CC mediate efficient cellular immune response interactions. In humans CD4 is
CC the target of interaction with the human immunodeficiency virus HIV. The
CC immunoglobulin is used to kill cells infected with HIV, and for treating
CC or preventing infection. It is also used for imaging HIV-infected tissues
CC (for staging or prognosis of infection, and for assessing efficacy of
CC treatments). The immunoglobulin is also used to determine the HIV
CC envelope glycoprotein burden, once determined, this information is used
CC in the staging and prognosis of HIV infected patients. The
CC immunoglobulin should be active against all strains of HIV (since the
CC CD4-PIG20 interaction is essential for infection). The heterotetramers
CC are assembled intracellularly and secreted efficiently from mammalian
CC cells, allowing high recovery and purification from the culture medium.
CC They have longer half-life in serum and greater avidity than heavy chain
CC dimers
XX
SQ Sequence 310 AA;

```

```

Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 2.8e-64;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

```

```

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKSIOFHKNSNOIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKSIOFHKNSNOIK 60
QY 61 ILGNQSFLLTKGPSKLNDRADSRSLMDQGNPFLIIKNLIKIEDSDTYICEVEDQKEEVL 120

```

```

DB 61 ILGNQSFLLTKGPSKLNDRADSRSLMDQGNPFLIIKNLIKIEDSDTYICEVEDQKEEVL 120
QY 121 LVFGLTANSDPTLLLOGSLTTLTSPGSSPSPVOCRRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDPTLLLOGSLTTLTSPGSSPSPVOCRRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEEKIDIVPPASALPAPPTGSALPDQOTASALPDPPAASALPALAVI 240
DB 181 TWTCTVLQNOQKVEEKIDIVVLAFTVAAP-----SVFIIPSPDEQLKSGTASV 228
QY 241 SFL 244
DB 229 VCIL 232

```

```

RESULT 5
AAB67324
ID AAB67324 standard; protein, 310 AA.
XX
AC AAB67324;
XX
DT 23-APR-2001 (first entry)
XX
DE CD4-kappa chimeric light chain protein.
XX
KM Immunoglobulin; chelator; chimeric; HIV; human immunodeficiency virus.
XX
OS Homo sapiens.
XX
PN US6177549-B1.
XX
PD 23-JAN-2001.
XX
PF 10-JUN-1999; 99US-00329916.
XX
PR 07-AUG-1992; 92US-00927931.
PR 06-AUG-1993; 93WO-US007422.
PR 03-FEB-1995; 95US-00379516.
PR 07-JUN-1995; 95US-00477460.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
PI Maddon PJ, Allway GP;
XX
DR MPI; 2001-158582/16.
XX
PT Immunoglobulin for treating human immunodeficiency virus-infected
PT subject, consists of cytotoxic radionuclide linked to heterotetramer
PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
PT kappa-light chains.
XX
PS Disclosure; Fig 5; 43pp; English.
XX
CC The present invention relates to an immunoglobulin, comprising a
CC cytotoxic radionuclide linked, directly or via a bifunctional chelator,
CC to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by
CC an expression vector CD4-IgG2HC-PRCMV and two chimeric CD4-kappa light
CC chains encoded by an expression vector CD4-KLC-PRCMV. The invention is
CC useful for killing human immunodeficiency virus (HIV)-infected cells, for
CC the treatment and prevention of infection with HIV
XX
SQ Sequence 310 AA;

```

```

Query Match 78.8%; Score 1038; DB 4; Length 310;
Best Local Similarity 85.7%; Pred. No. 2.8e-64;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

```

```

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKSIOFHKNSNOIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKSIOFHKNSNOIK 60
QY 61 ILGNQSFLLTKGPSKLNDRADSRSLMDQGNPFLIIKNLIKIEDSDTYICEVEDQKEEVL 120

```

```

Db      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFLLIKNLKIEDSDTYICEVEQKEVQL 120
Qy      121 LVFGLTANSPTHTLLQGSLTLLTLESPGSSPSVQCSPRGKNTGGKTLISVSQLELDQSG 180
Db      121 LVFGLTANSPTHTLLQGSLTLLTLESPGSSPSVQCSPRGKNTGGKTLISVSQLELDQSG 180
Qy      181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
Db      181 TWCTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVTFPPSDEQLKSGTASV 228
Qy      241 SFLL 244
Db      229 VCLL 232

RESULT 6
AAB80885
ID      AAB80885 standard; protein; 310 AA.
XX
AC      AAB80885;
XX
DT      29-MAY-2001 (first entry)
XX
DE      Human CD4-kappa chimeric light chain.
XX
KW      Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
        Immunoglobulin gamma 2; CD4-kappa.
XX
OS      Homo sapiens.
XX
PN      US6187748-B1.
XX
PD      13-FEB-2001.
XX
PF      07-JUN-1995; 95US-00485372.
XX
PR      08-FEB-1991; 91US-00653684.
PR      10-FEB-1992; 92MC-US001143.
PR      08-DEC-1992; 92US-00960440.
XX
PA      (PROG-) PROGENICS PHARM INC.
XX
PI      Maddon PJ, Beaudry GA;
XX
DR      WPI; 2001-264981/27.
XX
DR      N-PSDB; AAF77831.
XX
PT      Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
PT      or treating a subject having CD4+ cells infected with HIV involves using
PT      CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
XX
PS      Disclosure; Fig 5; 55pp; English.
XX
XX
XX      The present invention relates to a method for inhibiting infection of a
XX      CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
XX      chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
XX      differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface
XX      glycoprotein that is expressed primarily on the surface of T cells. In
XX      man, CD4 is the target of interaction with HIV. The heterotetramer has
XX      two heavy and two light chains which are encoded by expression vectors
XX      CC CD4-IgG2HC-PRCMV (V1) and CD4-kLC-PRCMV (V2), respectively. The method
XX      is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
XX      cells of a subject from becoming infected with HIV. The method is also
XX      useful for treating a subject having CD4+ cells infected with HIV. The
XX      present sequence is human fusion protein: CD4-kappa chimeric light chain
XX      CC of the CD4-IgG2 chimeric heterotetramer. This sequence was used in the
XX      method of the present invention
XX
PS      Sequence 310 AA;
XX
XX
XX      Query Match      78.8%; Score 1038; DB 4; Length 310;
XX      Best Local Similarity 85.7%; Pred. No. 2.8e-64;
XX      Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

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```

Qy      1 MNRGVPFRHLLVLQALILPAATQGNKVVLTGKKDVTVELTCTASOKKSIOFHKNSNOIK 60
Db      1 MNRGVPFRHLLVLQALILPAATQGNKVVLTGKKDVTVELTCTASOKKSIOFHKNSNOIK 60
Qy      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFLLIKNLKIEDSDTYICEVEQKEVQL 120
Db      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFLLIKNLKIEDSDTYICEVEQKEVQL 120
Qy      121 LVFGLTANSPTHTLLQGSLTLLTLESPGSSPSVQCSPRGKNTGGKTLISVSQLELDQSG 180
Db      121 LVFGLTANSPTHTLLQGSLTLLTLESPGSSPSVQCSPRGKNTGGKTLISVSQLELDQSG 180
Qy      181 TWCTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
Db      181 TWCTCTVLQNKQKVEFKIDIVLAFTVAAP-----SVTFPPSDEQLKSGTASV 228
Qy      241 SFLL 244
Db      229 VCLL 232

RESULT 7
ABG71124
ID      ABG71124 standard; protein; 310 AA.
XX
AC      ABG71124;
XX
DT      17-JAN-2003 (first entry)
XX
DE      CD4-kappa chimeric light chain of the CD4-IgG2 chimeric protein.
XX
KW      CD4; kappa light chain; human immunodeficiency virus-1; HIV-1; mutant;
        mutein.
XX
OS      Homo sapiens.
XX
PN      US6451313-B1.
XX
PD      17-SEP-2002.
XX
PF      07-JUN-1995; 95US-00484681.
XX
PR      08-FEB-1991; 91US-00653684.
PR      10-FEB-1992; 92MC-US001143.
PR      08-DEC-1992; 92US-00960440.
XX
PA      (PROG-) PROGENICS PHARM INC.
XX
PI      Maddon PJ, Beaudry GA;
XX
DR      WPI; 2003-038273/03.
XX
DR      N-PSDB; ABS55722.
XX
XX
XX      Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human
XX      PT immunodeficiency virus-1 with two heavy and light chains encoded by
XX      PT expression vectors designated CD4-IgG2HC-PRCMV and CD4-kLC-PRCMV,
XX      PT respectively.
XX
PS      Claim 1; Fig 5A-D; 54pp; English.
XX
XX
XX      The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric
XX      CC heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-
XX      CC 1) having two heavy chains encoded by an expression vector designated CD4
XX      -IgG2HC-PRCMV, and two light chains encoded by expression vector

```

CC designated CD4-KLc-PRCCMV. (I) and a composition (II) comprising (I) or
 CC (1) linked to a toxin, are useful for inhibiting HIV infection of a CD4
 CC cell, and preventing a subject being infected with HIV by blocking the
 CC spread of HIV infection. This is the amino acid sequence of the CD4-kappa
 CC chimeric light chain of the CD4-IgG2 chimeric heterotetramer useful in
 CC inhibiting HIV infection

XX
 SQ Sequence 310 AA;

Query Match 78.8%; Score 1038; DB 6; Length 310;
 Best Local Similarity 85.7%; Pred. No. 2.8e-64;
 Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVFPHLLIVLQALLPATQGNKVVLGKGGDTVELTCTASQKSIQFMKNSNOIK 60
 DB 1 MNRGVFPHLLIVLQALLPATQGNKVVLGKGGDTVELTCTASQKSIQFMKNSNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEYQL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEYQL 120
 QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWICTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPPPPASALPALAVI 240
 DB 181 TWICTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPPPPASALPALAVI 240
 QY 241 SFLL 244
 DB 229 VCLL 232

RESULT 8
 AAE37574
 ID AAE37574 standard; protein; 450 AA.

XX
 AC AAE37574;

XX
 DT 27-AUG-2003 (first entry)

XX
 DE Human D1D2-Ig alphacp fusion protein.

XX
 KM Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;

XX
 KM human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D1;

XX
 OS Homo sapiens.

XX
 PN WO2003040311-A2.

XX
 PD 15-MAY-2003.

XX
 PF 24-OCT-2002; 2002WO-US034393.

XX
 PR 25-OCT-2001; 2001US-0346231P.

XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Archos J, Cicala C, Fauci AS;

XX
 DR WPI; 2003-441545/41.

XX
 DR N-PSDB; AAD29113.

XX
 PT New CD4 polypeptide ligated at its C-terminus with a portion of an

XX
 PS preventing HIV-1 infection.

XX
 CC Example 1; Page 47; 100pp; English.

XX
 CC The invention relates to a CD4 (cluster of differentiation factor 4)

XX
 CC polypeptide ligated at its C-terminus with a portion of an immunoglobulin

CC (Ig) comprising a hinge region and a constant domain of a mammalian Ig
 CC heavy chain. The polypeptide comprises a tailpiece from the C-terminus of
 CC the heavy chain of an IGA or IGM antibody. Polypeptides of the invention
 CC are useful for preparing a composition for treating or preventing human
 CC immunodeficiency virus (HIV)-1 infection. The invention is useful in gene
 CC therapy and also in the preparation of vaccines. The present sequence is
 CC a fusion protein which comprises a human IgA alpha tailpiece (alphatp), a
 CC human IGG constant region comprising a hinge, a CH2 and CH3 region and a
 CC human CD4 D1D2 domain

XX
 SQ Sequence 450 AA;

Query Match 78.7%; Score 1036.5; DB 6; Length 450;
 Best Local Similarity 89.7%; Pred. No. 5.5e-64;
 Matches 208; Conservative 0; Mismatches 19; Indels 5; Gaps 1;

QY 1 MNRGVFPHLLIVLQALLPATQGNKVVLGKGGDTVELTCTASQKSIQFMKNSNOIK 60
 DB 1 MNRGVFPHLLIVLQALLPATQGNKVVLGKGGDTVELTCTASQKSIQFMKNSNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEYQL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDTYICEVEDQKEEYQL 120
 QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWICTVLQNKQKVEFKIDIVPRASA-----LPAPPTGSALPDPQTASALPDP 227
 DB 181 TWICTVLQNKQKVEFKIDIVPRASA-----LPAPPTGSALPDPQTASALPDP 227

RESULT 9
 AAR26531
 ID AAR26531 standard; protein; 534 AA.

XX
 AC AAR26531;

XX
 DT 25-MAR-2003 (revised)

XX
 DT 28-JAN-1993 (first entry)

XX
 DE Sequence of CD4-IgG1 chimeric heavy chain heterotetramer.

XX
 KM CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;

XX
 KM therapy; diagnostic agent; inhibition.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers

XX
 FT Region 205..302

XX
 FT Region /label= CH1

XX
 FT Region 303..317

XX
 FT Region /label= hinge

XX
 FT Region 318..427

XX
 FT Region /label= CH2

XX
 FT Region 428..534

XX
 FT Region /label= CH3

XX
 PN WO9213559-A1.

XX
 PD 20-AUG-1992.

XX
 PF 10-FEB-1992; 92WO-US001152.

XX
 PR 08-FEB-1991; 91US-00654205.

XX
 PA (PROG-) PROGENICS PHARM INC.

XX
 PI Beaudry GA, Madden PJ;

XX
 DR WPI; 1992-299758/36.

XX
 DR N-PSDB; AAO27831.


```
XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT for preventing and creating HIV infection useful as a diagnostic agent.
XX
XX Example; Fig 4; 89pp; English.
XX
CC The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into
CC M13mp18. In order to excise a fragment containing the CH1 exon of the
CC human gamma 1 heavy chain gene, the plasmid pSP gamma 1 is digested with
CC SacII, and the SacII sites are then made flush using T4 DNA polymerase.
CC The fragment containing the CH1 exon is then purified and ligated to the
CC M13mp18(CD4) vector. Oligonucleotide-mediated site-directed mutagenesis
CC is then performed to juxtapose the CD4 and CH1 sequences in frame. The
CC CD4-CH1 chimeric gene is then linearized and ligated to the pSP6T4 DNA
CC fragment of the plasmid pSP gamma 1 containing the hinge, CH2, and CH3
CC exons of the human gamma 1 chain gene designated CD4-IgG1HC-pSP6T4 (ATCC
CC 75192). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 534 AA;
Query Match 78.4%; Score 1033; DB 2; Length 534;
Best Local Similarity 85.7%; Pred. No. 1.2e-63;
Matches 209; Conservative 3; Mismatches 10; Indels 22; Gaps 3;
QY 1 MNRGVPRHLLVQLALPAAATQGNKVVGKKGDVLTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAAATQGNKVVGKKGDVLTCTASOKKSIQFHKNSNQIK 60
QY 61 ILNGQSFLLTKGSPKLNDRADSRSLMDQGNFPLIINKLIEPDTYICEVEDQKEVOL 120
DB 61 ILNGQSFLLTKGSPKLNDRADSRSLMDQGNFPLIINKLIEPDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPDTHLLQGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPDTHLLQGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQOKKVEFKIDIVLAFASTKGSVPFLAPSSKSTSGGTALGLVKDYFPEP 240
DB 181 TWTCTVLOQOKKVEFKIDIVLAFASTKGSVPFLAPSSKSTSGGTALGLVKDYFPEP 240
QY 219 QTAS 222
DB 241 VTVS 244
RESULT 10
AAR26782
ID AAR26782 standard; protein; 432 AA.
XX
AC AAR26782;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 06-FEB-1993 (first entry)
XX
DE CD4-gamma2 chimeric heavy chain homodimer.
XX
KW homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS Homo sapiens.
OS Chimeric.
XX
FH Key
FH Domain 1. .216
FH Domain /label= CD4
FH Domain 217. 325
FH Domain /label= CH2
FH Domain 326. 433
FH Domain /label= CH3
XX
XX WO9213947-A1.
```

```
PD 20-AUG-1992.
XX
XX 10-FEB-1992; 92MO-US001143.
XX
XX 08-FEB-1991; 91US-00653684.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Beaudry GA, Maddon PJ;
XX
XX WPI; 1992-300034/36.
XX
XX N-PSDB; AAQ28088.
XX
PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT treatment, prevention and diagnosis of HIV infection.
XX
XX Claim 2; Fig 3; 90pp; English.
XX
CC This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It
CC was produced by expression of the coding mutagenised cDNA (produced as
CC described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently
CC assembled intracellularly and effectively secreted from mammalian cells
CC pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery
CC and purification from the medium of cells expressing it. It possesses
CC increased serum half-life and has increased avidity for HIV cf. heavy
CC chain dimers. It can inhibit HIV infection of CD4+ cells and block the
CC spread of HIV infection within a patient. Attachment to a detectable
CC marker makes it useful in an assay for HIV or SIV infection, and it can
CC also be linked to toxins, eg diphtheria, pseudomonas exotoxin A (domains
CC I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003
CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 432 AA;
Query Match 78.4%; Score 1032.5; DB 2; Length 432;
Best Local Similarity 88.0%; Pred. No. 9.9e-64;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;
QY 1 MNRGVPRHLLVQLALPAAATQGNKVVGKKGDVLTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAAATQGNKVVGKKGDVLTCTASOKKSIQFHKNSNQIK 60
QY 61 ILNGQSFLLTKGSPKLNDRADSRSLMDQGNFPLIINKLIEPDTYICEVEDQKEVOL 120
DB 61 ILNGQSFLLTKGSPKLNDRADSRSLMDQGNFPLIINKLIEPDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPDTHLLQGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPDTHLLQGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQOKKVEFKIDIVLAFASTKGSVPFLAPSSKSTSGGTALGLVKDYFPEP 240
DB 181 TWTCTVLOQOKKVEFKIDIVLAFASTKGSVPFLAPSSKSTSGGTALGLVKDYFPEP 240
RESULT 11
AAR46678
ID AAR46678 standard; protein; 432 AA.
XX
AC AAR46678;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1994 (first entry)
XX
DE CD4-gamma 2 chimeric heavy chain.
XX
XX CD4; gamma; heavy chain; chimeric; chimeric; immunocjugate; HIV;
XX human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
XX imaging; detection; targeting.
XX
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
```



```

Db      121 LVFGLTANSDFHLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY      181 TWTCVTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTQTASALPDPPAA 230
        |||||
Db      181 TWTCVTVLQNKQKVEFKIDIVLAFERKCCVECP-----CPAPPVA 221

RESULT 15
ABG71122
ID      ABG71122 standard; protein; 432 AA.
XX
AC      ABG71122;
XX
DT      17-JAN-2003 (first entry)
XX
DE      CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric protein.
XX
KW      CD4; gamma2 heavy chain; human immunodeficiency virus-1; HIV-1; mutant;
        mutant.
XX
OS      Homo sapiens.
XX      Synthetic.
XX
FH      Key
        Location/Qualifiers
FT      Peptide
        1..25
        /label= Signal_peptide
FT      Protein
        26..432
        /note="mature CD4-gamma2 chimeric heavy chain of the CD4
        -IgG2 chimeric heterotetramer"
XX
XX      US6451313-B1.
XX
PN      17-SEP-2002.
XX
PD      07-JUN-1995; 95US-00484681.
XX
PF      08-FEB-1991; 91US-00653684.
XX
PR      10-FEB-1992; 92WO-US001143.
PR      08-DEC-1992; 92US-00960440.
XX
PA      (PROG-) PROGENICS PHARM INC.
XX
PI      Maddon PJ, Beaudry GA;
XX
DR      WPI; 2003-038273/03.
XX
DR      N-PSDB; ABSS5720.
XX
XX
PT      Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human
        immunodeficiency virus-1 with two heavy and light chains encoded by
        expression vectors designated CD4-IgG2HC-PRCMV and CD4-KLC-PRCMV,
        respectively.
XX
PS      Disclosure; Fig 3A-F; 54pp; English.
XX
XX
CC      The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric
        heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-
        1) having two heavy chains encoded by an expression vector designated CD4
        -IGG2HC-PRCMV, and two light chains encoded by expression vector
        designated CD4-KLC-PRCMV. (I) and a composition (II) comprising (I) or
        (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4
        cell, and preventing a subject being infected with HIV by blocking the
        spread of HIV infection. This is the amino acid sequence of the CD4-
        gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer
        useful in inhibiting HIV infection
XX
SQ      Sequence 432 AA;

Query Match      78.4%; Score 1032.5; DB 6; Length 432;
Best Local Similarity 88.0%; Pred. No. 9,9e-64;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY      1 MNRGVPFRHLLVLQALLPAAATQGNKTVLGKKGDTVELTCTASQKKSIOFHMKNNOIK 60
        |||||

```

```

Db      1 MNRGVPFRHLLVLQALLPAAATQGNKTVLGKKGDTVELTCTASQKKSIOFHMKNNOIK 60
QY      61 ILGNQGSFLLTGKPSKLNDRADSRRLMDQGNPFLIKKLTEDSPDYICEVEDQEEVQL 120
        |||||
Db      61 ILGNQGSFLLTGKPSKLNDRADSRRLMDQGNPFLIKKLTEDSPDYICEVEDQEEVQL 120
        |||||

QY      121 LVFGLTANSDFHLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
Db      121 LVFGLTANSDFHLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY      181 TWTCVTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTQTASALPDPPAA 230
        |||||
Db      181 TWTCVTVLQNKQKVEFKIDIVLAFERKCCVECP-----CPAPPVA 221

RESULT 16
AAR26783
ID      AAR26783 standard; protein; 530 AA.
XX
AC      AAR26783;
XX
DT      24-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      06-FEB-1993 (first entry)
XX
DE      CD4-IgG2 chimeric heavy chain.
XX
KW      homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
        chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
XX      Homo sapiens.
XX      Chimeric.
XX
OS      Homo sapiens.
XX
FH      Key
        Location/Qualifiers
FT      Domain
        1..205
        /label= CD4 domain
FT      Domain
        206..302
        /label= CH1 domain
FT      Domain
        303..312
        /label= hinge domain
FT      Domain
        313..423
        /label= CH2 domain
FT      Domain
        424..530
        /label= CH3 domain
XX
PN      WO9213947-A1.
XX
PD      20-AUG-1992.
XX
PF      10-FEB-1992; 92WO-US001143.
XX
PR      08-FEB-1991; 91US-00653684.
XX
PA      (PROG-) PROGENICS PHARM INC.
XX
PI      Beaudry GA, Maddon PJ;
XX
DR      WPI; 1992-300034/36.
XX
DR      N-PSDB; AAQ28089.
XX
XX
PT      CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
        treatment, prevention and diagnosis of HIV infection.
XX
PS      Claim 15; Fig 4; 90pp; English.
XX
XX
CC      This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer
        CC it was produced by expression of the coding mutagenised cDNA (produced as
        CC described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently
        CC assembled intracellularly and effectively secreted from mammalian cells
        CC pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high
        CC recovery and purification from the medium of cells expressing it. It
        CC possesses increased serum half-life and has increased avidity for HIV cf.
        CC heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block

```

CC the spread of HIV infection within a patient. Attachment to a detectable
 CC marker makes it useful in an assay for HIV or SIV infection, and it can
 CC also be linked to toxins, eg Diphtheria, Pseudomonas exotoxin A (domains
 CC I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003
 CC to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 530 AA;

Query Match 78.2%; Score 1030.5; DB 2; Length 530;
 Best Local Similarity 84.8%; Pred. No. 1,7e-63;
 Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
 DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCSPRGKNIQGGKTLSSVSOLELQDSG 180
 DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCSPRGKNIQGGKTLSSVSOLELQDSG 180
 QY 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
 DB 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
 QY 241 SFTL 244
 DB 230 GCLV 233

RESULT 17
 AAY85080
 ID AAY85080 standard; protein; 530 AA.

XX AAY85080;

XX 19-JUN-2000 (first entry)

XX CD4-IgG2 chimeric heterotetramer heavy chain amino acid sequence.

XX CD4-IgG2 chimeric heavy chain heterotetramer; immunocjugate; treatment;
 KM cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
 KM cellular immune response interaction mediator; HIV interaction; staging;
 KM prognosis; envelope glycoprotein burden; human.

XX Homo sapiens.

XX US6034223-A.

XX 07-MAR-2000.

XX 07-JUN-1995; 95US-00477460.

XX 07-AUG-1992; 92US-00927931.

XX 06-AUG-1993; 93WO-US007422.

XX 03-FEB-1995; 95US-00379516.

XX (PROG-) PROGENICS PHARM INC.

XX Allaway GP, Maddon PJ;

XX WPI; 2000-269502/23.

XX N-PSDB; AA298856.

XX New immunocjugate, used to treat, prevent or image human immune
 PT deficiency virus infection, comprises radionuclide attached to
 PT heterotetramer of CD4-immunoglobulin chimeras.

XX Disclousure; Fig 4; 58pb; English.

CC This sequence represents the CD4-IgG2 chimeric heavy chain amino acid
 CC sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates
 CC to an immunocjugate comprising a cytotoxic radionuclide and a
 CC heterotetramer of two heavy chains and two light chains. The cytotoxic
 CC radionuclide is linked to either the heavy chains or the light chains, or
 CC to all four chains, directly or through a bifunctional chelator. Both
 CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
 CC vector CD4-IgG2HC-PRCMV (ATCC 75193) and both light chains are chimeric
 CC CD4-kappa chains encoded by vector CD4-kLC-pRCMV (ATCC 75194). CD4 is a
 CC non-polymorphic cell surface glycoprotein that is expressed on the
 CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
 CC and dendritic cells. CD4 associates with major histocompatibility complex
 CC (MHC) class II molecules on the surface of antigen presenting cells to
 CC mediate efficient cellular immune response interactions. In humans CD4 is
 CC the target of interaction with the human immunodeficiency virus HIV. The
 CC immunocjugate is used to kill cells infected with HIV, and for treating
 CC or preventing infection. It is also used for imaging HIV-infected tissues
 CC (for staging or prognosis of infection, and for assessing efficacy of
 CC treatments). The immunocjugate is also used to determine the HIV
 CC envelope glycoprotein burden, once determined, this information is used
 CC in the staging and prognosis of HIV infected patients. The
 CC immunocjugate should be active against all strains of HIV (since the
 CC CD4-gp120 interaction is essential for infection). The heterotetramers
 CC are assembled intracellularly and secreted efficiently from mammalian
 CC cells, allowing high recovery and purification from the culture medium.
 CC They have longer half-life in serum and greater avidity than heavy chain
 CC dimers
 CC
 XX
 SQ Sequence 530 AA;

Query Match 78.2%; Score 1030.5; DB 3; Length 530;
 Best Local Similarity 84.8%; Pred. No. 1,7e-63;
 Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
 DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCSPRGKNIQGGKTLSSVSOLELQDSG 180
 DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCSPRGKNIQGGKTLSSVSOLELQDSG 180
 QY 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
 DB 181 TWTCTVLQNGKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
 QY 241 SFTL 244
 DB 230 GCLV 233

RESULT 18
 AAB67323
 ID AAB67323 standard; protein; 530 AA.

XX AAB67323;

XX 23-APR-2001 (first entry)

XX CD4-IgG2 chimeric heavy chain protein.

XX Immunocjugate; chelator; chimeric; HIV; human immunodeficiency virus.

XX Homo sapiens.

XX US6177549-B1.

XX 23-JAN-2001.

PF 10-JUN-1999; 99US-00329916.
XX
XX 07-AUG-1992; 92US-00927931.
PR 06-FEB-1993; 93MO-US007422.
PR 03-FEB-1995; 95US-00379516.
PR 07-JUN-1995; 95US-00477460.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Maddon PJ, Allaway GP;
XX WPI; 2001-158582/16.
XX
XX Immunodeficiency for treating human immunodeficiency virus-infected
PT subject, consists of cytotoxic radionuclide linked to heterotetramer
PT comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
PT kappa/light chains.
XX
XX Disclosure; Fig 4; 43pp; English.
XX
XX The present invention relates to an immunoconjugate, comprising a
CC cytotoxic radionuclide linked, directly or via a bifunctional chelator,
CC to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by
CC an expression vector CD4-IgG2HC-PRCMV and two chimeric CD4-kappa light
CC chains encoded by an expression vector CD4-kLC-PRCMV. The invention is
CC useful for killing human immunodeficiency virus (HIV)-infected cells, for
CC the treatment and prevention of infection with HIV
XX
XX Sequence 530 AA;
SQ
Query Match 78.2%; Score 1030.5; DB 4; Length 530;
Best Local Similarity 84.8%; Pred. No. 1.7e-63;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;
QY 1 MNRGVPFRHLLVLTALPAATQGNKVVLTGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPFRHLLVLTALPAATQGNKVVLTGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILNGQSFLLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEEYOL 120
DB 61 ILNGQSFLLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEEYOL 120
QY 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
DB 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
QY 181 TWTCTVLQONQKVEFKIDIVPAASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWTCTVLQONQKVEFKIDIVPAASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233
RESULT 19
ID AAB80884 standard; protein; 530 AA.
XX AAB80884;
XX
XX 29-MAY-2001 (first entry)
XX
XX Human CD4-IgG2 chimeric heavy chain.
DE
XX Human; Anti-HIV; CD4-IgG2 chimeric heterotetramer;
KM Immunoglobulin gamma 2.
XX
XX Homo sapiens.
OS
XX US6187748-B1.
PN
XX 13-FEB-2001.
PD

XX
XX 07-JUN-1995; 95US-00485372.
XX
XX 08-FEB-1991; 91US-00653684.
PR 10-FEB-1992; 92MO-US001143.
PR 08-DEC-1992; 92US-00960440.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Maddon PJ, Beaudry GA;
XX WPI; 2001-264981/27.
XX
XX N-PSDB; AAF77830.
XX
XX Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell,
PT or treating a subject having CD4+ cells infected with HIV involves using
PT CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
XX
XX Disclosure; Fig 4; 55pp; English.
XX
XX The present invention relates to a method for inhibiting infection of a
CC CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
CC chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of
CC differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface
CC glycoprotein that is expressed primarily on the surface of T cells. In
CC man, CD4 is the target of interaction with HIV. The heterotetramer has
CC two heavy and two light chains which are encoded by expression vectors
CC CD4-IgG2HC-PRCMV (VI) and CD4-kLC-PRCMV (V2), respectively. The method
CC is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+
CC cells of a subject from becoming infected with HIV. The method is also
CC useful for treating a subject having CD4+ cells infected with HIV. The
CC present sequence is human fusion protein: CD4-Ig2 chimeric heavy chain of
CC the CD4-Ig2 chimeric heterotetramer. This sequence was used in the
CC method of the present invention
XX
XX Sequence 530 AA;
SQ
Query Match 78.2%; Score 1030.5; DB 4; Length 530;
Best Local Similarity 84.8%; Pred. No. 1.7e-63;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;
QY 1 MNRGVPFRHLLVLTALPAATQGNKVVLTGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPFRHLLVLTALPAATQGNKVVLTGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILNGQSFLLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEEYOL 120
DB 61 ILNGQSFLLTKGSPSKLNDRAISRSLMDQGNPFLIIKNLKIETSDPTVYICEVEDQKEEYOL 120
QY 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
DB 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
QY 181 TWTCTVLQONQKVEFKIDIVPAASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWTCTVLQONQKVEFKIDIVPAASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233
RESULT 20
ID ABG71123 standard; protein; 530 AA.
XX ABG71123;
XX
XX 17-JAN-2003 (first entry)
XX
XX CD4-immunoglobulin G2 (IgG2) chimeric heterotetramer.
DE
XX CD4; immunoglobulin G2; Ig gamma2; human immunodeficiency virus-1; HIV-1;
XX


```
XX CD4 D1-D2 domains.
DE
XX
XX CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IGL;
KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KW dendritic cell; therapy; mammal; infection.
XX Homo sapiens.
XX MO9603883-A1.
XX
XX 15-FEB-1996.
XX
XX 26-JUL-1995; 95MO-US009468.
XX PF
XX 02-AUG-1994; 94US-00284391.
XX PR
XX 24-FEB-1995; 95US-00394388.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B, Banapour B, Romeo C, Kolanus W;
XX
XX WPI; 1996-129034/13.
XX DR
XX N-PSDB; AAT10738.
XX
XX Membrane-bound chimeric receptor comprising extracellular portion
PT including CD4 fragment - cells expressing receptor can be used for
PT treatment of HIV infection.
XX
XX Example 10; Fig 24; 134pp; English.
XX
XX This sequence represents the CD4 D1-D2 domains of CD4. This sequence is
CC included in the membrane bound proteinaceous chimeric receptor of the
CC invention. The extracellular portion of the chimeric receptor contains a
CC fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which
CC specifically recognises and binds HIV-infected cells, but does not
CC mediate HIV infection. The extracellular domain of the receptor is
CC separated from the cell membrane by 48 or 72 angstroms, or by one or more
CC proteinaceous alpha-helices. The transmembrane region of the chimeric
CC receptor contains a portion of the CD7, CD5 or CD34 transmembrane domain.
CC Alternatively, the extracellular portion of the receptor can also be
CC separated from the intracellular domain by the hinge, CH2 and CH3 domains
CC of human IgL. The cells expressing the receptor are preferably T cells,
CC B cells, neutrophils, or dendritic cells. The therapeutic cells
CC expressing the chimeric receptor are administered to a mammal to treat
CC HIV infection
CC
XX
XX Sequence 203 AA;
SQ
Query Match 78.1%; Score 1029; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.5e-64;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKKGDVLTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKKGDVLTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQSFLLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQSFLLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSDTHLLQGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200
```

RESULT 23
AAR78673
ID AAR78673 standard; protein; 398 AA.

```
XX AAR78673;
AC
XX 12-APR-1996 (first entry)
XX
XX CD4 domains D1-D4.
XX
XX Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis;
KM human immunodeficiency virus; adoptive immunotherapy.
XX
XX Homo sapiens.
XX
XX WO9521528-A1.
XX PN
XX 17-AUG-1995.
XX PD
XX 12-JAN-1995; 95MO-US000454.
XX PF
XX 14-FEB-1994; 94US-00195395.
XX PR
XX 02-AUG-1994; 94US-00284391.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B, Banapour B, Romeo C, Kolanus W;
XX
XX WPI; 1995-292893/38.
XX DR
XX N-PSDB; AAQ96103.
XX
XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
PT cells.
PT
XX
XX Example 10; Fig 23; 118pp; English.
XX
XX Extracellular domains D1-D4 (AAR78673) or D1-D2 (AAR78674) of human CD4
CC are used in the construction of chimeric receptors utilised in the
CC targeted cytolysis of cells expressing HIV envelope proteins on their
CC surface. The chimeric receptors comprise the extracellular domain (pref.
CC amino acids 1-394 or 1-200) of CD4 linked to an intracellular portion,
CC e.g. of T-cell receptor protein zeta
CC
XX
XX Sequence 398 AA;
SQ
Query Match 78.1%; Score 1029; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.6e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKKGDVLTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRFRLHLVQLALPAATQGNKVVLGKKGDVLTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQSFLLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQSFLLTKGSPSKLNDRAISRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSDTHLLQGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200
```

RESULT 24
AAR89450
ID AAR89450 standard; peptide; 398 AA.
XX
XX AAR89450;
XX
XX 26-SEP-1996 (first entry)
XX
XX CD4 D1-D4 domains.
XX

KM CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
 KM human; CD4; HIV; proteoglycan alpha-helix; T cell; B cell; neutrophil;
 KM dendritic cell; therapy; mammal; infection.
 OS Homo sapiens.
 XX WO603883-A1.
 XX PN
 XX 15-FEB-1996.
 PD
 XX 26-JUL-1995; 95MO-US009468.
 PF
 XX 02-AUG-1994; 94US-00284391.
 PR 24-FEB-1995; 95US-00394388.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 XX Seed B, Banapour B, Romeo C, Kolanus W;
 PI
 XX WPI; 1996-129034/13.
 DR N-PSDB; AAT10797.
 DR
 XX
 PT Membrane-bound chimeric receptor comprising extracellular portion
 PT including CD4 fragment - cells expressing receptor can be used for
 PT treatment of HIV infection.
 XX
 PS Example 10; Fig 23; 134pp; English.
 XX
 CC This sequence represents the D1-D4 domains of CD4. This sequence is
 CC included in the membrane bound proteoglycan chimeric receptor of the
 CC invention. The extracellular portion of the chimeric receptor contains a
 CC fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which
 CC specifically recognises and binds HIV-infected cells, but does not
 CC mediate HIV infection. The extracellular domain of the receptor is
 CC separated from the cell membrane by 48 or 72 angstroms, or by one or more
 CC proteoglycan alpha-helices. The transmembrane region of the chimeric
 CC receptor contains a portion of the CD7, CD5 or CD34 transmembrane domain.
 CC Alternatively, the extracellular portion of the receptor can also be
 CC separated from the intracellular domain by the hinge, CH2 and CH3 domains
 CC of human IgG1. The cells expressing the receptor are preferably T cells,
 CC B cells, neutrophils, or dendritic cells. The therapeutic cells
 CC expressing the chimeric receptor are administered to a mammal to treat
 CC HIV infection.
 CC
 XX
 SQ Sequence 398 AA;
 Query Match 78.1%; Score 1029; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHKNSNQIK 60
 DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHKNSNQIK 60
 QY 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOQGSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180
 DB 121 LVFGLTANSPTHLLOQGSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVLQNKQKVEFKIDIV 200
 RESULT 25
 AAR06374
 ID AAR06374 standard; protein; 400 AA.
 XX
 AC AAR06374;
 XX

DT 31-OCT-2002 (revised)
 DT 20-DEC-1990 (first entry)
 XX
 DE Truncated form of soluble T4 encoded by PBG381.
 KM
 KM plasmid PBG381; soluble T4 protein; AIDS; ARC; HIV.
 XX
 OS Synthetic.
 FH
 FT Key
 FT Peptide
 FT 1. .23
 FT /label= secretory signal
 FT /note= "hydrophobic"
 FT 24. .117
 FT Region
 FT /label= extracellular
 FT /note= "homology to V-regions"
 FT 118. .132
 FT Region
 FT /label= extracellular
 FT /note= "homology to J-regions"
 FT 133. .397
 FT Region
 FT /label= extracellular
 FT /note= "glycosylated"
 FT
 XX WO9008198-A.
 XX
 XX 26-JUL-1990.
 PD
 XX 18-JAN-1989; 89US-00300096.
 PF
 XX 18-JAN-1989; 89US-00300096.
 PR 18-JAN-1989; 89US-00300096.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Letvin NA;
 XX
 XX WPI; 1990-254040/33.
 DR N-PSDB; AAQ05608.
 DR
 XX
 PT Treating or preventing AIDS, ARC or HIV infection - by administering an
 PT immunologically effective amt. of soluble T4 protein.
 XX
 PS Disclosure; Fig 2; 121pp; English.
 CC
 CC T4-encoding plasmid PBG381 was used to transform Chinese Hamster Ovary
 CC cells for the production of truncated T4. Soluble T4 is produced by
 CC virtue of the removal of the transmembrane and cytoplasmic domains. The
 CC soluble forms may be modified to increase their immunogenicity by
 CC addition of an adjuvant such as incomplete Freund's adjuvant. The T4
 CC interferes with HIV/T4 interaction and elicits anti-soluble T4 antibody
 CC production. See also AAQ05607. (Updated on 31-OCT-2002 to add missing OS
 CC field.)
 CC
 XX
 SQ Sequence 400 AA;
 Query Match 78.1%; Score 1029; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHKNSNQIK 60
 DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKDVTVELTCTASQKKSIOFHKNSNQIK 60
 QY 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOQGSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180
 DB 121 LVFGLTANSPTHLLOQGSLLTLTSPGSSPSVQCRSPRGKNIQGGKTLSSVQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 26

AAP91922 standard; protein; 402 AA.

AAP91922;

AC 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 14-MAY-1990 (first entry)

Sequence of a secreted form of the CD4 adhesion (CD4T) polypeptide.

CD4 variants; CD4T, gp120, plasmid pRCD4, HIV-1, HTLV-IIIB.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 25..26 /note="signal processing site"

FT Misc-difference 366 /note="other forms of CD4T terminate here"

FT Misc-difference 368 /note="other forms of CD4T terminate here"

EP314317-A.

03-MAY-1989.

03-OCT-1988; 88EP-00309194.

02-OCT-1987; 87US-00104329.

28-SEP-1988; 88US-00250785.

(GENTH) GENENTECH INC.

Capron DJ, Gregory TJ;

WPI; 1989-111855/18.

N-PSDB; AAN90777.

Compens. contg. adhesion variants - useful in therapy and diagnostics, e.g. CD4 variants which are therapeutically useful for treating human

immuno-deficiency virus.

Disclosure; Fig 1a-1c; 36pp; English.

PS It may be capable of binding gp120. It may be fused with an
 CC immunoglobulin constant domain, human transferrin, apolipoprotein,
 CC albumin, ricin A chain or diphtheria toxin A. It may be used for
 CC antiviral of immunomodulatory therapy particularly in treatment of HIV
 CC infection. It may have variants by insertion, substitution of deletion in
 CC non-functional regions. (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PI field.)
 CC
 XX

Sequence 402 AA;

Query Match 78.1%; Score 1029; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVLTQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNNSNOIX 60
 DB 1 MNRGVPFRHLLVLTQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNNSNOIX 60

QY 61 ILNGQGSFLTKGSPKLNDRADSRSLMDQGNPFLIITKNLKIENSDPTIYICVEDQKEEVOU 120
 DB 61 ILNGQGSFLTKGSPKLNDRADSRSLMDQGNPFLIITKNLKIENSDPTIYICVEDQKEEVOU 120

QY 121 LVFGLTANSPTHLILQGSQSLTLTLESPPGSSPVQCSPRGKNIQGGKTLVSQLELDQSG 180
 |||

DB 121 LVFGLTANSPTHLILQGSQSLTLTLESPPGSSPVQCSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWICTVLONOKKVEFKIDIV 200
 DB 181 TWICTVLONOKKVEFKIDIV 200

RESULT 27

AAP94757 standard; protein; 402 AA.

AAP94757;

AC 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 28-JAN-1991 (first entry)

Sequence of a secreted form of the CD4 adhesion.

HIV; antiviral; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers

FT Peptide 1..25 /note="signal"

FT Protein 26..402

W08902922-A.

06-APR-1989.

03-OCT-1988; 88WO-US003414.

02-OCT-1987; 87US-00104329.

28-SEP-1988; 88US-00250785.

(GENTH) GENENTECH INC.

Capron DJ, Gregory TJ;

WPI; 1989-114397/15.

N-PSDB; AAN90734.

New nucleic acid sequences encoding adhesion. esp. CD 4, variants -

partic. with trans-membrane domain inactivated or fused to other peptide,

useful esp. for treating HIV infections.

Disclosure; Fig 1a-1c; 78pp; English.

PS The patent claims a nucleic acid encoding an aa sequence variant of an
 CC adhesion, which is pref. a CD4 polypeptide variant modified such that its
 CC transmembrane domain has been inactivated, either deleted or replaced by
 CC a sequence of hydrophilic hydrophathy profile. The aa sequence variant of
 CC an adhesion may also be a fusion of CD4 with a 2nd polypeptide esp. one
 CC contg. a non-CD4 epitope; a signal sequence; a cpd. able to elicit a
 CC humoral immune response (viral polypeptide or allergen); or a human
 CC plasma protein of long plasma half-life. CD4 fusion proteins can have
 CC antiviral and immunomodulatory activity and are esp. useful for treating
 CC HIV infections regardless of genetic variation within the virus. They and
 CC antibodies raised against them can also be used diagnostically for
 CC assaying adhesions and their ligands. (Updated on 03-OCT-2002 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.)
 CC
 XX

Sequence 402 AA;

Query Match 78.1%; Score 1029; DB 1; Length 402;
 Best Local Similarity 100.0%; Pred. No. 1.6e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVLTQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHKNNSNOIX 60
 |||

```

Db      1 MNRGVPFRHLVLVQLALPAAATQGNKVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
QY      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIEISDPTIICEVEDQKEEVOL 120
        61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIEISDPTIICEVEDQKEEVOL 120
QY      121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
        121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
Db      121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
QY      181 TWTCVTVLQONOKKVEFKIDIV 200
        181 TWTCVTVLQONOKKVEFKIDIV 200
Db      181 TWTCVTVLQONOKKVEFKIDIV 200

RESULT 28
AAP91990
ID      AAP91990 standard; protein; 458 AA.
XX
AC      AAP91990;
XX
DT      25-MAR-2003 (revised)
DT      15-OCT-1990 (first entry)
XX
DE      Clone pT4B encoded HIV T4 glycoprotein.
XX
KM      Human Immunodeficiency Virus T4 envelope glycoprotein; AIDS; ss.
OS      Synthetic.
XX
FH      Key
FT      Peptide
        1. .23
        /label= leader peptide
        24. .117
        /label= variable-like region 1
        118. .134
        /label= joining-like region 1
        135. .189
        /label= variable-like region 2
        190. .205
        /label= joining-like region 2
        206. .287
        /label= variable-like region 3
        288. .309
        /label= joining-like region 3
        297. .299
        /label= putative N-glycosylation site
        310. .377
        /label= variable-like region 4
        325. .327
        /label= putative N-glycosylation site
        378. .397
        /label= joining-like region 4
        398. .420
        /label= trans-membrane region
        421. .458
        /label= cytoplasmic region
XX
PN      WC0801304-A.
XX
PD      25-FEB-1988.
XX
PF      20-AUG-1987; 87MO-US002050.
XX
PR      21-AUG-1986; 86US-00898587.
XX
PA      (UYCO-) COLUMBIA UNIV.
PA      (MADD/) MADDON P J.
XX
PI      Litman DR, Maddon PJ, Chess L, Axel R, Weiss R, McDougall JS,
XX      WPI; 1986-064019/09.
XX      N-PSDB; AAN80512.
DR

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XX      XX
PT      Nucleic acid encoding T4 glyco:protein - used for treatment of AIDS and
PT      producing antibodies for use as vaccine for immunisation against AIDS.
XX      PS
XX      Disclosure; Page 7; 128pp; English.
XX      CC
XX      T4 protein encoded by part of 3kb insert from human T cell library
CC      (pT4B). (Updated on 25-MAR-2003 to correct PA field.)
XX      SO
        Sequence 458 AA;
        Query Match      78.1%; Score 1029; DB 1; Length 458;
        Best Local Similarity 100.0%; Pred. No. 1.8e-63;
        Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNRGVPFRHLVLVQLALPAAATQGNKVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
        1 MNRGVPFRHLVLVQLALPAAATQGNKVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
Db      61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIEISDPTIICEVEDQKEEVOL 120
        61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIINKLIEISDPTIICEVEDQKEEVOL 120
QY      121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
        121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
Db      121 LVFGLTANSDPTHLHQGSQSLTLTLESPPGSSPSVQCRRSPRGKNIQGKTLSSVQLLEQDSG 180
QY      181 TWTCVTVLQONOKKVEFKIDIV 200
        181 TWTCVTVLQONOKKVEFKIDIV 200
Db      181 TWTCVTVLQONOKKVEFKIDIV 200

RESULT 29
AAP91369
ID      AAP91369 standard; protein; 458 AA.
XX
AC      AAP91369;
XX
DT      24-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      08-JAN-1990 (first entry)
XX
DE      T4 protein.
XX
KM      T4 protein; human immunodeficiency virus; AIDS; clone pT4B.
OS      Homo sapiens; (human).
XX
FH      Key
FT      Domain
        1. .23
        24. .117
        41
        109
        118. .134
        135. .189
        155
        184
        190. .204
        205. .286
        287. .309
        296. .298
        310. .376
        325. .327
        328
        370
        377. .397
        398. .420
        421. .458
XX
PN      EPJ30227-A.
XX
PD      30-AUG-1989.
XX

```



```

DT 03-DEC-1999 (first entry)
XX
DE Soluble human T4 protein.
XX
KM Soluble T4 protein; gT4; human; HIV; binding inhibitor; T4+ cell; AIDS;
XX vaccine; immunization; therapy.
XX
OS Homo sapiens.
XX
FN US5958678-A.
XX
PD 28-SEP-1999.
XX
PF 12-DEC-1994; 94US-00354452.
XX
PR 21-AUG-1986; 86US-00898587.
XX 11-JUN-1991; 91US-00713564.
XX 06-JUL-1992; 92US-00909021.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI McDougal JS, Weiss R, Axel R, Littman DR, Maddon PJ, Chess L;
XX WPI; 1999-561025/47.
XX
DR N-PSDB; AAZ20695.
XX
PT Human T4 protein inhibits HIV binding to T4 cells, useful for treating
XX AIDS.
XX
PS Example 3; Fig 6; 58pp; English.
XX
CC This sequence represents the soluble human T4 protein of the invention.
XX The soluble human T4 protein blocks the binding of HIV to T4+ cells and
XX is therefore useful for the treatment of AIDS. Monoclonal antibodies
XX against the T4 protein may be used as vaccines for immunising subjects
XX against AIDS
XX
SQ Sequence 458 AA;

Query Match 78.1%; Score 1029; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRRLILVQLALPPAATQGNKVVLGKGDVETLTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRRLILVQLALPPAATQGNKVVLGKGDVETLTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLLTKGSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
DB 61 ILGNQGSFLLTKGSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLLOGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLONQKVEFKIDIV 200
DB 181 TWTCTVLONQKVEFKIDIV 200

RESULT 32
AAB07769
ID AAB07769 standard; protein; 458 AA.
XX
AC AAB07769;
XX
DT 07-NOV-2000 (first entry)
XX
DE DNA encoding a human T4 glycoprotein.
XX
KM Human; T4 glycoprotein; human immunodeficiency virus; HIV;
XX envelope glycoprotein; AIDS; virus binding.
XX

```

```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /note= "leader sequence"
FT Modified-site 296..298
FT /note= "N-linked glycosylation site"
FT Modified-site 325..327
FT /note= "N-linked glycosylation site"
FT Domain 398..420
FT /note= "Transmembrane domain"
FT FT 421..458
FT /note= "cytoplasmic domain"
XX
PN US6093539-A.
XX
PD 25-JUL-2000.
XX
PF 06-JUN-1995; 95US-00466368.
XX
PR 21-AUG-1986; 86US-00898587.
XX 11-JUN-1991; 91US-00713564.
XX 06-JUL-1992; 92US-00909021.
XX 12-DEC-1994; 94US-00354452.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Maddon PJ, Chess L, Weiss R, McDougal JS, Littman DR;
XX WPI; 2000-505203/45.
XX
DR N-PSDB; AAA59352.
XX
PT New isolated nucleic acid encoding a human T cell surface protein and the
XX soluble surface T4 glycoprotein that it encodes, useful as prophylaxis
XX for treating a subject infected with human acquired immune deficiency
XX syndrome virus.
XX
PS Disclosure; Fig 6A-B; 69pp; English.
XX
CC The present sequence represents a human T4 glycoprotein. An aqueous-
XX soluble polypeptide comprising a portion of a human T4 glycoprotein
XX specifically forms a complex with a human immunodeficiency virus (HIV)
XX envelope glycoprotein. The DNA is useful for producing the soluble
XX surface T4 glycoprotein. The soluble surface T4 glycoprotein is useful
XX as a therapeutic agent, i.e. as prophylaxis for treating a subject infected
XX with an HIV virus. Thus, the soluble T4 glycoprotein is also useful in
XX treating human AIDS. The soluble T4 glycoprotein is also useful in
XX diagnostic or screening assays, e.g. for screening inhibitors of virus
XX binding, or for detecting and quantitating T4, T4+ cells and antibodies
XX to T4, which are of diagnostic value for AIDS
XX
SQ Sequence 458 AA;

Query Match 78.1%; Score 1029; DB 3; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.8e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRRLILVQLALPPAATQGNKVVLGKGDVETLTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRRLILVQLALPPAATQGNKVVLGKGDVETLTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLLTKGSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
DB 61 ILGNQGSFLLTKGSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLLOGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOGOSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLONQKVEFKIDIV 200
DB 181 TWTCTVLONQKVEFKIDIV 200

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RESULT 33
AAR27277
ID AAR27277 standard; protein; 462 AA.
XX
XX AAR27277;
XX
DT 25-MAR-2003 (revised)
DT 28-JUL-1995 (first entry)
XX
DE CD4:eta peptide chimeric protein.
XX
XX Fusion protein; CD4; extracellular domain; zeta; eta; gamma;
XX membrane spanning domain; intracellular domain; type I;
XX integral membrane homodimer; TCR; T cell antigen receptor;
XX extracellular domain; mouse; human; receptor; chimera;
XX HBB-ALU tumour cell line; natural killer cell.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Protein 1..399
FT /note="CD4 extracellular domain"
FT Protein 400..462
FT /note="Zeta membrane spanning and intracellular domain"
XX
XX W09215322-A1.
XX
XX 17-SEP-1992.
XX
XX 06-MAR-1992; 92MO-US001785.
XX
XX 07-MAR-1991; 91US-00665961.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Seed B, Romeo C, Kolanus W;
XX
XX WPI; 1992-331474/40.
XX
XX N-PSDB; AAQ28705.
XX
XX Therapeutic cells expressing chimeric receptors - directing cellular
XX response to an infective agent, useful in treating HIV-1, AIDS
XX
XX Pneumocystis carinii infections etc.
XX
XX
XX Example 2; Page 73-74; 114pp; English.
XX
XX This sequence represents a fusion protein between the CD4 extracellular
XX domain and the eta protein membrane spanning domain and intracellular
XX domain. Eta is an isoform of zeta (see also AAR27276) which is a 32 kD
XX type I integral membrane homodimer, which arises by alternate mRNA
XX splicing. It is present in reduced amounts in cells expressing the T cell
XX antigen receptor. Zeta-eta heterodimers are thought to mediate the
XX formation of inositol phosphates, as well as the receptor initiated cell
XX death called apoptosis, in the production of the CD4 receptor chimera,
XX the eta cDNA was isolated from the HBB-ALU tumour cell line and from
XX human natural killer cells. The eta cDNA was joined to the extracellular
XX domain of an engineered form of CD4 possessing a BamHI site just upstream
XX of the membrane spanning domain, by a BamHI site naturally present a few
XX residues upstream of the membrane spanning domain. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 462 AA;
XX
Query Match 78.1%; Score 1029; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
```

```

DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
QY 121 LVFGLTANSDBTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDBTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200

RESULT 34
AAR78677
ID AAR78677 standard; protein; 462 AA.
XX
XX AAR78677;
XX
XX 16-APR-1996 (first entry)
XX
XX T-cell receptor gamma.
XX
XX Chimeric receptor; CD4; T-cell receptor gamma; HIV; cytolysis;
XX human immunodeficiency virus; adoptive immunotherapy.
XX
XX Homo sapiens.
XX
XX W09521528-A1.
XX
XX 17-AUG-1995.
XX
XX 12-JAN-1995; 95WO-US000454.
XX
XX 14-FEB-1994; 94US-00195395.
XX
XX 02-AUG-1994; 94US-00284391.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Seed B, Banapour B, Romeo C, Kolanus W;
XX
XX WPI; 1995-292893/38.
XX
XX P-PSDB; AAQ96123.
XX
XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
XX cells.
XX
XX Example 2; Page 77-78; 118pp; English.
XX
XX Fusion proteins comprising the extracellular domain of CD4 fused to T-
XX cell receptor zeta, gamma or eta (AAR78676-78, respectively) were
XX expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma
XX and CD4:eta chimeric receptors mediated cytolysis of targets expressing
XX HIV gp120/41
XX
XX Sequence 462 AA;
XX
Query Match 78.1%; Score 1029; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKKGDTVELCTASOKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVL 120
QY 121 LVFGLTANSDBTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDBTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
```

```

Db      181 TWTCVTVLQNGKVKVEFKIDIV 200
|||||
RESULT 35
AAR89457
ID AAR89457 standard; protein; 462 AA.
XX
AC AAR89457;
XX
DT 26-SEP-1996 (first entry)
XX
DE CD4:gamma fusion protein.
XX
KW CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
KM dendritic cell; therapy; mammal; infection.
XX
OS Synthetic.
XX
PN W09603883-A1.
XX
PD 15-FEB-1996.
XX
PF 26-JUL-1995; 95WO-US009468.
XX
PR 02-AUG-1994; 94US-00284391.
XX
PR 24-FEB-1995; 95US-00394388.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B, Banapour B, Romeo C, Kolanus W;
XX
DR WPI; 1996-129034/13.
XX
DR N-PSDB; AAT10802.
XX
PT Membrane-bound chimeric receptor comprising extracellular portion
PT including CD4 fragment - cells expressing receptor can be used for
PT treatment of HIV infection.
XX
XX
XX
PS Example 2; Page 79; 134pp; English.
XX
CC AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors
CC of the invention. This sequence represents the CD4:gamma chimera. The
CC transmembrane region of the chimeric receptor acts to separate the
CC intracellular and extracellular domains of the chimera, and contains a
CC portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains.
CC Alternatively, the extracellular portion of the receptor can be separated
CC from the intracellular domain by the hinge, CH2 and CH3 domains of human
CC IgG1 (see AAR89441). The extracellular portion of the chimeric receptor
CC contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
CC sequence, see AAR89450 and AAR89451) which specifically recognizes and
CC binds HIV-infected cells, but does not mediate HIV infection. The
CC extracellular domain of the receptor is separated from the cell membrane
CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The
CC cells expressing the receptor are preferably T cells, B cells,
CC neutrophils, or dendritic cells. The therapeutic cells expressing the
CC chimeric receptor are administered to a mammal to treat HIV infection
XX
SQ Sequence 462 AA;
Query Match 78.1%; Score 1029; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.9e-53;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLTLVQLALLPAATGKNKVLGKGDVTELTCTASQKKSIOPHMNSNQIK 60
DB 1 MNRGVPFRHLTLVQLALLPAATGKNKVLGKGDVTELTCTASQKKSIOPHMNSNQIK 60
QY 61 ILNGSGFLTKGPKSLMDRADSRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILNGSGFLTKGPKSLMDRADSRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVOL 120

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QY 121 LVFGLTRANSDTHLQGSQSLTLTLESPGSSPSVQCSPRGKNIQGGKTLVSQLEHODSG 180
DB 121 LVFGLTRANSDTHLQGSQSLTLTLESPGSSPSVQCSPRGKNIQGGKTLVSQLEHODSG 180
QY 181 TWTCVTVLQNGKVKVEFKIDIV 200
DB 181 TWTCVTVLQNGKVKVEFKIDIV 200
RESULT 36
AAW02214
ID AAW02214 standard; protein; 462 AA.
XX
AC AAW02214;
XX
DT 11-NOV-1996 (first entry)
XX
DE CD4:Fc receptor gamma chain chimeric receptor.
XX
KW Chimeric receptor; cellular immunity; adoptive immunotherapy; CD4;
KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;
KM Fc receptor gamma chain; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Domain 1..393
FT /label= "Extracellular_domain"
FT /note= "CD4 extracellular domain"
FT 394..397
FT /label= "Linker"
FT /note= "encoding DNA contains a BamHI site used for
FT fusion construction"
FT Region 398..462
FT /note= "region of fusion derived from gamma chain,
FT preferred signal-transducing portions for constructs of
FT the invention are amino acids 421-462 and 402-419"
FT Domain 400..462
FT /label= "Transmembrane+intracellular_domains"
XX
PN W09625953-A1.
XX
PD 29-AUG-1996.
XX
PF 25-JAN-1996; 96WO-US001056.
XX
PR 24-FEB-1995; 95US-00394176.
XX
PA (GEHO ) GEN HOSPITAL CORP.
XX
PI Seed B, Romeo C, Kolanus W;
XX
DR WPI; 1996-402134/40.
XX
DR N-PSDB; AAT36759.
XX
PT Direction of cellular immune response using therapeutic cell expressing 2
PT chimeric receptors - comprising region binding to target cell and region
PT that signals target cell destruction, or CD28 region, partic. for
PT eliminating HIV-infected cells.
XX
PS Claim 7; Page 76; 120pp; English.
XX
XX
XX A chimeric receptor (AAW02214) comprises the extracellular domain of an
XX engineered form of the CD4 cellular receptor for HIV and the
XX transmembrane and intracellular regions, including the cytoytic signal-
XX transducing portion, of the human Fc receptor gamma chain; the region of
XX the fusion is shown in AAW02223. It can be obtd. by inserting a gene
XX fusion (AAT36759) into a vaccinia virus vector and expression in host
XX cells. Chimeric receptors comprising CD4 fused to Fc receptor gamma or T
XX cell receptor zeta (see also AAW02213) or eta (AAW02215) chains are
XX capable of directing cytotoxic T lymphocytes to specifically recognise
XX and kill cells expressing HIV gp120, thus providing a therapy for AIDS

```

SQ Sequence 462 AA;
 Query Match 78.1%; Score 1029; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60
 DB 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60
 QY 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYVL 120
 DB 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYVL 120
 QY 121 LVFGLTANSDDTHLLGGOSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSDDTHLLGGOSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKVKVEPKIDIV 200
 DB 181 TWTCTVLQNKVKVEPKIDIV 200

RESULT 37
 AAW83142
 ID AAW83142 standard; protein: 462 AA.
 AC AAW83142;
 DT 03-FEB-1999 (first entry)
 DE Chimeric receptor containing mouse gamma polypeptide.
 XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;
 KM tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;
 KM CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
 KM protozoan; viral.
 OS Synthetic.
 XX Mus sp.
 PN US5843728-A.
 PD 01-DEC-1998.
 PF 05-APR-1995; 95US-00417495.
 PR 07-MAR-1991; 91US-00665961.
 PR 06-MAR-1992; 92US-00847566.
 PR 28-FEB-1994; 94US-00203866.
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 PI Romeo C, Kolanus W, Seed B;
 DR WPI; 1999-044582/04.
 DR N-PSDB; AAV70158.
 XX Membrane-bound chimeric receptors - comprising extracellular portion
 PT which recognises and binds a target cell and an intracellular portion of
 PT e.g. a T-cell receptor.
 XX
 PS Example 2; Col 43-46; 57pp; English.

CC or autoimmune-generated cells
 XX
 SQ Sequence 462 AA;
 Query Match 78.1%; Score 1029; DB 2; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1.9e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60
 DB 1 MNRGVPRHLLVLTALLPATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNOIK 60
 QY 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYVL 120
 DB 61 ILNGQSFLLTKGPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEYVL 120
 QY 121 LVFGLTANSDDTHLLGGOSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSDDTHLLGGOSLTTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKVKVEPKIDIV 200
 DB 181 TWTCTVLQNKVKVEPKIDIV 200

RESULT 38
 AAR27278
 ID AAR27278 standard; protein: 532 AA.
 AC AAR27278;
 DT 25-MAR-2003 (revised)
 DT 28-JUL-1995 (first entry)
 DE CD4; gamma peptide chimeric protein.
 XX Fusion protein; CD4; extracellular domain; zeta; eta; gamma;
 KM membrane spanning domain; intracellular domain; type I;
 KM integral membrane homodimer; TCR; T cell antigen receptor;
 KM extracellular domain; mouse; human; receptor; chimera;
 KM HPB-ALL tumour cell line; natural killer cell.
 OS Homo sapiens.
 PN WO9215322-A1.
 PD 17-SEP-1992.
 PF 06-MAR-1992; 92WO-US001785.
 PR 07-MAR-1991; 91US-00665961.
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 PI Seed B, Romeo C, Kolanus W;
 DR WPI; 1992-331474/40.
 DR N-PSDB; AAQ28706.
 XX Therapeutic cells expressing chimeric receptors - directing cellular
 PT response to an infective agent, useful in treating HIV-1, AIDS
 PT Pneumocystis carinii infections etc.
 XX
 PS Example 2; Page 74-76; 114pp; English.

This sequence represents a fusion protein between the CD4 extracellular
 domain and the gamma protein membrane spanning domain and intracellular
 domain. The Fc-receptor-associated gamma chain is expressed in cell
 surface complexes with additional polypeptides, some of which mediate
 ligand recognition, and others which have undefined function. Gamma bears
 a homodimeric structure and overall organisation very similar to that of
 zeta (see also AAQ28704), and is a component of both the mast
 cell/basophil high affinity IgE receptor, Fc-epsilon-RI, which consists

CC of at least three distinct polypeptide chains and one of the low affinity
 CC receptors for IgG, represented in mice by Fc-gamma-R11-alpha. In the
 CC production of the CD4 receptor chimera, the gamma cDNA was isolated from
 CC the HBB-MuL tumour cell line and from human natural killer cells. The
 CC gamma cDNA was joined to the extracellular domain by engineering a BamHI
 CC site just upstream of the membrane spanning domain, by a BamHI site
 CC naturally present a few residues upstream of the membrane spanning
 CC domain. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2,2e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHKNSNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEVOL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEVOL 120
 QY 121 LVFGLTANSDTHLLQGQSLTLTLSPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSDTHLLQGQSLTLTLSPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
 QY 181 TWICTVLQONOKKVEFKIDIV 200
 DB 181 TWICTVLQONOKKVEFKIDIV 200

RESULT 39

AAR78678 standard; protein; 532 AA.

XX AAR78678;

DT 16-APR-1996 (first entry)

XX T-cell receptor eta.

XX Chimeric receptor; CD4; T-cell receptor eta; HIV; cytolysis;

KM human immunodeficiency virus; adoptive immunotherapy.

OS Homo sapiens.

XX MO9521528-A1.

XX 17-AUG-1995.

XX 12-JAN-1995; 95W0-US000454.

XX 14-FEB-1994; 94US-00193395.

XX 02-AUG-1994; 94US-00284391.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Banapour B, Romeo C, Kolanus W;

XX WPI; 1995-292893/38.

XX N-PSDB; AAQ96124.

XX Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
 PT cells.

XX Example 2; Page 78-79; 118pp; English.

CC Fusion proteins comprising the extracellular domain of CD4 fused to T-
 CC cell receptor zeta, gamma or eta (AAR78676-78, respectively) were
 CC expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma
 CC and CD4:eta chimeric receptors mediated cytolysis of targets expressing
 CC HIV gp120/41

XX Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2,2e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLILVQLALLPAATQGNKVVLGKKGDVLTCTASQKKSIOFHKNSNOIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEVOL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRAISRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEVOL 120
 QY 121 LVFGLTANSDTHLLQGQSLTLTLSPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSDTHLLQGQSLTLTLSPGSSPSVQCRSPRGKNIQGKTLVSQLELDQSG 180
 QY 181 TWICTVLQONOKKVEFKIDIV 200
 DB 181 TWICTVLQONOKKVEFKIDIV 200

RESULT 40

AAR89458 standard; protein; 532 AA.

XX AAR89458;

DT 26-SEP-1996 (first entry)

XX CD4:eta fusion protein.

XX CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
 KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
 KM dendritic cell; therapy; mammal; infection.

XX Synthetic.

XX MO9603883-A1.

XX 15-FEB-1996.

XX 26-JUL-1995; 95W0-US009468.

XX 02-AUG-1994; 94US-00284391.

XX 24-FEB-1995; 95US-00394388.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Banapour B, Romeo C, Kolanus W;

XX WPI; 1996-129034/13.

XX N-PSDB; AAT10803.

PT Membrane-bound chimeric receptor comprising extracellular portion
 PT including CD4 fragment - cells expressing receptor can be used for
 PT treatment of HIV infection.

XX Example 2; Page 80-81; 134pp; English.

CC AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors
 CC of the invention. This sequence represents the CD4:eta chimera. The
 CC transmembrane region of the chimeric receptor acts to separate the
 CC intracellular and extracellular domains of the chimera, and contains a
 CC portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains.
 CC Alternatively, the extracellular portion of the receptor can be separated
 CC from the intracellular domain by the hinge, CH2 and CH3 domains of human
 CC IgG1 (see AAR89441). The extracellular portion of the chimeric receptor
 CC contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
 CC sequence, see AAR89450 and AAR89451) which specifically recognises and
 CC binds HIV-infected cells, but does not mediate HIV infection. The

CC extracellular domain of the receptor is separated from the cell membrane
 CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The
 CC cells expressing the receptor are preferably T cells, B cells,
 CC neutrophils, or dendritic cells. The therapeutic cells expressing the
 CC chimeric receptor are administered to a mammal to treat HIV infection
 XX
 SQ Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2.2e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKSNQIK 60
 DB 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKSNQIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
 QY 121 LVFGLTANSPTHTLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHTLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQONOKKVEFKIDIV 200
 DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 41
 AAM02215
 ID AAM02215 standard; protein; 532 AA.
 XX
 AC AAM02215;

XX 16-OCT-2003 (revised)
 DT 11-NOV-1996 (first entry)

XX CD4:T-cell receptor eta chain chimeric receptor.

XX Chimeric receptor: cellular immunity; adoptive immunotherapy; CD4;
 KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;
 KM T-cell receptor eta chain; cytotoxic T lymphocyte; CTL.

XX Homo; sapiens.
 OS Mus sp.
 OS Chimeric.

PH Key Location/Qualifiers
 FT Domain 1..393

FT /label= "Extracellular domain"
 FT /note= "CD4 extracellular domain"
 FT 394..396

FT Region /label= linker
 FT /note= "encoding DNA contains a BamHI site used for
 FT fusion construction"
 FT 397..532

FT /note= "region of fusion derived from eta chain,
 FT preferred signal-transducing portions for constructs of
 FT the invention are amino acids 421-532, 423-455, 438-455,
 FT 461-494, 494-528 or 400-420"

FT Domain 400..437

FT /label= "Transmembrane domain"

FT /note= "eta chain transmembrane domain"

FT Domain 438..575

FT /label= "Intracellular domain"

XX /note= "eta chain intracellular domain"

PN MO9625953-A1.

XX 29-AUG-1996.

PD 25-JAN-1996; 96MO-US001056.

XX 24-FEB-1995; 95US-00394176.
 PR (GEHO) GEN HOSPITAL CORP.
 XX
 PA
 XX Seed B, Romeo C, Kolanus W;
 PI
 XX WPI; 1996-402134/40.
 DR N-PSDB; AAT36760.

PT Direction of cellular immune response using therapeutic cell expressing 2
 PT chimeric receptors - comprising region binding to target cell and region
 PT that signals target cell destruction, or CD28 region, partic. for
 PT eliminating HIV-infected cells.

PS Claim 7, Page 77-78; 120pp; English.

XX A chimeric receptor (AAM00215) comprises the extracellular domain of an
 CC engineered form of the CD4 cellular receptor for HIV and the
 CC transmembrane and intracellular regions, including the cytosolic signal-
 CC transducing portion, of the mouse T-cell receptor eta chain. It can be
 CC obtd. by inserting a gene fusion (AAT36760) into a vaccinia virus vector
 CC and expression in host cells. Chimeric receptors comprising CD4 fused to
 CC eta, eta (see also AAM02213) or Fc receptor gamma (see also AAM02214)
 CC chains are capable of directing cytotoxic T lymphocytes to specifically
 CC recognise and kill cells expressing HIV gp120, thus providing a therapy
 CC for AIDS. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2.2e-63;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKSNQIK 60
 DB 1 MNRGVPFRHLVLTQALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHWKSNQIK 60
 QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
 DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120
 QY 121 LVFGLTANSPTHTLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHTLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQONOKKVEFKIDIV 200
 DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 42
 AAM83141
 ID AAM83141 standard; protein; 532 AA.
 XX
 AC AAM83141;

XX 03-FEB-1999 (first entry)

XX Chimeric receptor containing human eta polypeptide.

XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;
 KM tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;
 KM CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
 KM protozoan; viral.

XX Synthetic.
 OS Homo sapiens.

XX US5843728-A.

PD 01-DEC-1998.

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PF 05-APR-1995; 95US-00417495.
XX
PR 07-MAR-1991; 91US-00665961.
PR 06-MAR-1992; 92US-00847566.
PR 28-FEB-1994; 94US-00203866.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
PI Romeo C, Kolanus W, Seed B;
XX
XX WPI; 1999-044582/04.
DR N-PSDB; AAV70157.
XX
XX Membrane-bound chimeric receptors - comprising extracellular portion
PT which recognizes and binds a target cell and an intracellular portion of
PT e.g. a T-cell receptor.
XX
XX Claim 11; Col 45-48; 57pp; English.
XX
XX The present invention describes DNA encoding a membrane-bound chimeric
CC receptor comprising: (a) an extracellular portion that specifically
CC recognizes and binds a target cell or a target infective agent; and (b)
CC an intracellular portion of a T-cell receptor CD3, zeta or eta
CC polypeptide, a B-cell receptor polypeptide or an FC receptor polypeptide.
CC The present sequence represents a chimeric receptor containing the human
CC eta polypeptide. Cells expressing chimeric receptors of the present
CC invention can be administered to mammals in order to destroy pathogens
CC (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
CC or autoimmune-generated cells
XX
SQ Sequence 532 AA;

Query Match 78.1%; Score 1029; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 2.2e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60

QY 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGGSLTTLTLESPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGGSLTTLTLESPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180

QY 181 TWTCTVLQONOKKVEFKIDIV 200
DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 43
AAR27276
ID AAR27276 standard; protein; 575 AA.
XX
XX AAR27276;
AC
XX
DT 25-MAR-2003 (revised)
DT 28-JUL-1995 (first entry)
XX
XX CD4: zeta peptide chimeric protein.
DE
XX
XX Fusion protein; CD4; extracellular domain; zeta; eta; gamma;
XX membrane spanning domain; intracellular domain; type I;
XX integral membrane homodimer; TCR; T cell antigen receptor;
XX extracellular domain; mouse; human; receptor; chimera;
XX HBB-ALL tumour cell line; natural killer cell.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH

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FT Protein 1..399
FT /note="CD4 extracellular domain"
FT Protein 400..575
FT /note="Zeta membrane spanning and intracellular domain"
XX
XX MO9215322-A1.
XX
XX 17-SEP-1992.
XX
XX PD
XX
XX PF 06-MAR-1992; 92MO-US001785.
XX
XX PR 07-MAR-1991; 91US-00665961.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Seed B, Romeo C, Kolanus W;
XX
XX WPI; 1992-331474/40.
DR N-PSDB; AAQ28704.
XX
XX Therapeutic cells expressing chimeric receptors - directing cellular
PT response to an infective agent, useful in treating HIV-1, AIDS
PT Pneumocystis carinii infections etc.
XX
XX Example 2; Page 72-73; 114pp; English.
XX
XX This sequence represents a fusion protein between the CD4 extracellular
CC domain and the zeta protein membrane spanning domain and intracellular
CC domain. Zeta is a 32 kD type I integral membrane homodimer which has a 9
CC residue extracellular domain and a 112/113 residue intracellular domain
CC for mouse and human protein respectively. In the production of the CD4
CC receptor chimera, the zeta cDNA was isolated from the HBB-ALL tumour cell
CC line and from human natural killer cells. The zeta cDNA was joined to the
CC extracellular domain of an engineered form of CD4 possessing a BamHI site
CC just upstream of the membrane spanning domain. By a BamHI site naturally
CC present a few residues upstream of the membrane spanning domain. (updated
CC on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 575 AA;

Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHWKNSQIK 60

QY 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTQKSPSKLNDRADSRSLWDOGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120

QY 121 LVFGLTANSDTHLLQGGSLTTLTLESPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGGSLTTLTLESPGSSPSVQCRSPRGKNIOGKTLVSQLELDQSG 180

QY 181 TWTCTVLQONOKKVEFKIDIV 200
DB 181 TWTCTVLQONOKKVEFKIDIV 200

RESULT 44
AAR78676
ID AAR78676 standard; protein; 575 AA.
XX
XX AAR78676;
AC
XX
DT 16-APR-1996 (first entry)
DT
XX
XX T-cell receptor zeta.
DE
XX
XX Chimeric receptor; CD4; T-cell receptor zeta; HIV; cytolysis;
XX human immunodeficiency virus; adoptive immunotherapy.
XX

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```
XX OS Homo sapiens.
XX XX
XX PN MO9521528-A1.
XX XX
XX PD 17-AUG-1995.
XX PF 12-JAN-1995; 95WO-US000454.
XX PR 14-FEB-1994; 94US-00195395.
XX PR 02-AUG-1994; 94US-00284391.
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Seed B, Banapour B, Romeo C, Kolanus W;
XX WPI; 1995-292893/38.
XX DR N-PSDB; AAQ96122.
XX PT Target cytolysis of HIV-infected cells - by chimeric CD4 receptor-bearing
XX PT cells.
XX PS Example 2; Page 76-77; 118pp; English.
XX CC Fusion proteins comprising the extracellular domain of CD4 fused to T-
XX CC cell receptor zeta, gamma or eta (AAR78676-78, respectively) were
XX CC expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma
XX CC and CD4:eta chimeric receptors mediated cytolysis of targets expressing
XX CC HIV gp120/41
XX SQ Sequence 575 AA:
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNSNQIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIIKNLKIEDSPYICGEVDQKEEVL 120
DB 61 ILGNQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIIKNLKIEDSPYICGEVDQKEEVL 120
QY 121 LVFGLTANSPTHTLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
DB 121 LVFGLTANSPTHTLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 45
AAR89456
ID AAR89456 standard; protein; 575 AA.
XX
XX AAR89456;
AC
XX
XX 26-SEP-1996 (first entry)
XX
XX CD4:zeta fusion protein.
XX
XX CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1;
XX KM human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
XX KM dendritic cell; therapy; mammal; infection.
XX
XX OS Synthetic.
XX
XX PN MO9603883-A1.
XX
XX PD 15-FEB-1996.
XX
```

```
PF 26-JUL-1995; 95WO-US009468.
XX
XX PR 02-AUG-1994; 94US-00284391.
XX PR 24-FEB-1995; 95US-00394388.
XX XX
XX PA (GENO ) GEN HOSPITAL CORP.
XX PI Seed B, Banapour B, Romeo C, Kolanus W;
XX WPI; 1996-129034/13.
XX DR N-PSDB; AAT10801.
XX PT Membrane-bound chimeric receptor comprising extracellular portion
XX PT including CD4 fragment - cells expressing receptor can be used for
XX PT treatment of HIV infection.
XX PS Example 2; Page 77-78; 134pp; English.
XX
XX CC AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors
XX CC of the invention. This sequence represents the CD4:zeta chimera. The
XX CC transmembrane region of the chimeric receptor acts to separate the
XX CC intracellular and extracellular domains of the chimera, and contains a
XX CC portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domain.
XX CC Alternatively, the extracellular portion of the receptor can be separated
XX CC from the intracellular domain by the hinge, CH2 and CH3 domains of human
XX CC IgG1 (see AAR89441). The extracellular portion of the chimeric receptor
XX CC contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4
XX CC sequence, see AAR89450 and AAR89451) which specifically recognises and
XX CC binds HIV-infected cells, but does not mediate HIV infection. The
XX CC extracellular domain of the receptor is separated from the cell membrane
XX CC by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The
XX CC cells expressing the receptor are preferably T cells, B cells,
XX CC neutrophils, or dendritic cells. The therapeutic cells expressing the
XX CC chimeric receptor are administered to a mammal to treat HIV infection
XX
XX SQ Sequence 575 AA:
XX
Query Match 78.1%; Score 1029; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.4e-63;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNSNQIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIIKNLKIEDSPYICGEVDQKEEVL 120
DB 61 ILGNQGSFLTKGPKSKLNDRADSRSLMDQGNPPLIIKNLKIEDSPYICGEVDQKEEVL 120
QY 121 LVFGLTANSPTHTLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
DB 121 LVFGLTANSPTHTLQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 46
AAW02213
ID AAW02213 standard; protein; 575 AA.
XX
XX AAW02213;
AC
XX
XX 11-NOV-1996 (first entry)
XX
XX CD4:T-cell receptor zeta chain chimaeric receptor.
XX
XX Chimaeric receptor; cellular immunity; adoptive immunotherapy; CD4;
XX KM human immunodeficiency virus type 1; HIV-1; AIDS; therapy;
XX KM T-cell receptor zeta chain; cytotoxic T lymphocyte; CTL.
XX
XX OS Homo sapiens.
```

```
XX Key Location/Qualifiers
FH Domain 1..393
FT /label= "Extracellular domain"
FT /note= "CD4 extracellular domain"
FT Region 394..396
FT /label= Linker
FT /note= "encoding DNA contains a BamHI site used for
FT fusion construction"
FT Region 397..575
FT /note= "region of fusion derived from zeta chain,
FT preferred signal-transducing portions for constructs of
FT the invention are amino acids 421-575, 423-255, 438-455,
FT 461-494, 494-528, 400-420 and 421-462"
FT Domain 400..437
FT /label= Transmembrane_domain
FT /note= "zeta chain transmembrane domain"
FT Domain 438..575
FT /label= Intracellular domain
FT /note= "zeta chain intracellular domain"
XX
XX MO9625953-A1.
XX
XX 29-AUG-1996.
XX
XX 25-JAN-1996; 96WO-US001056.
XX
XX 24-FEB-1995; 95US-00394176.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B, Romeo C, Kolanus W;
XX
XX WPI: 1996-402134/40.
XX N-PSDB; AAT36758.
XX
XX Direction of cellular immune response using therapeutic cell expressing 2
XX chimeric receptors - comprising region binding to target cell and region
XX that signals target cell destruction, or CD28 region, partic. for
XX eliminating HIV-infected cells.
XX
XX Claim 7; Page 74-75; 120pp; English.
XX
XX A chimeric receptor (AAW02213) comprises the extracellular domain of an
XX engineered form of the CD4 cellular receptor for HIV and the
XX transmembrane and intracellular regions, including the cytolytic signal-
XX transducing portion, of the human T-cell receptor zeta chain; the region
XX of the fusion is shown in AAW02221. It can be obtd. by inserting a gene
XX fusion (AAT36758) into a vaccinia virus vector and expression in host
XX cells. Chimeric receptors comprising CD4 fused to zeta, eta (see also
XX AAW02215) or Fc receptor gamma (see also AAW02214) chains are capable of
XX directing cytotoxic T lymphocytes to specifically recognise and kill
XX cells expressing HIV gp120, thus providing a therapy for AIDS
XX
XX Sequence 575 AA;
XX
XX Query Match 78.1%; Score 1029; DB 2; Length 575;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-63;
XX Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKGGDTVELCTASQKKSIOFHKNSNQIK 60
XX |
XX 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKGGDTVELCTASQKKSIOFHKNSNQIK 60
XX |
XX 1 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 61 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 61 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
XX |
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
XX |
XX 181 TWICTVLQNGKKEFKIDIV 200
XX |
```

```
DB 181 TWICTVLQNGKKEFKIDIV 200
|||||
RESULT 47
AAW83140
ID AAW83140 standard; protein; 575 AA.
XX
XX AAW83140;
XX
XX 03-FEB-1999 (first entry)
XX
XX Chimeric receptor containing human zeta polypeptide.
XX
XX Human; zeta; eta; gamma; membrane-bound chimeric receptor; infection;
XX tumour; cancer cell; autoimmune-generated cell; T cell receptor; CD3;
XX CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
XX protozoan; viral.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5843728-A.
XX
XX 01-DEC-1998.
XX
XX 05-APR-1995; 95US-00417495.
XX
XX 07-MAR-1991; 91US-00665961.
XX
XX 06-MAR-1992; 92US-00847566.
XX
XX 28-FEB-1994; 94US-00203866.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Romeo C, Kolanus W, Seed B;
XX
XX WPI: 1999-044582/04.
XX N-PSDB; AAW70156.
XX
XX Membrane-bound chimeric receptors - comprising extracellular portion
XX which recognises and binds a target cell and an intracellular portion of
XX e.g. a T-cell receptor.
XX
XX Example 2; Col 39-42; 57pp; English.
XX
XX The present invention describes DNA encoding a membrane-bound chimeric
XX receptor comprising: (a) an extracellular portion that specifically
XX recognises and binds a target cell or a target infective agent; and (b)
XX an intracellular portion of a T-cell receptor CD3, zeta or eta
XX polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide.
XX The present sequence represents a chimeric receptor containing the human
XX zeta polypeptide. Cells expressing chimeric receptors of the present
XX invention can be administered to mammals in order to destroy pathogens
XX (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
XX or autoimmune-generated cells
XX
XX Sequence 575 AA;
XX
XX Query Match 78.1%; Score 1029; DB 2; Length 575;
XX Best Local Similarity 100.0%; Pred. No. 2,4e-63;
XX Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKGGDTVELCTASQKKSIOFHKNSNQIK 60
XX |
XX 1 MNRGVPRHLLVQLALLPAATQGNKVVLGKGGDTVELCTASQKKSIOFHKNSNQIK 60
XX |
XX 1 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 61 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 61 ILGNQSFLLTKGPKSLNDRADSRSLWDQGNFPLIINKLKIEDSDTYICEVEDQKEVOL 120
XX |
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
XX |
XX 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDG 180
XX |
XX 181 TWICTVLQNGKKEFKIDIV 200
XX |
```

QY 181 TWTCVTLQNKVKVEFKIDIV 200
 |||||
 DB 181 TWTCVTLQNKVKVEFKIDIV 200

RESULT 48

AA04032
 ID AAR04032 standard; protein; 2037 AA.

XX AAR04032;

AC 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 29-MAY-1990 (first entry)

XX Full length T4 encoded by plasmid PBG381.

XX Soluble T4; PBG381; anti-retroviral agent; AIDS; ARC; HIV; AZT.

XX Synthetic.

XX WO8911860-A.

XX 14-DEC-1989.

XX 08-JUN-1989; 89MO-US002453.

XX 10-JUN-1988; 88US-00204645.

XX 20-APR-1989; 89US-00341080.

XX (BIOJ) BIOGEN NV INC.

XX (GEHO) GEN HOSPITAL CORP.

XX (BIOJ) BIOGEN INC.

XX (BIOJ) BIOGEN INC.

XX Fisher RA, Schooley RT, Hirsch MS, Johnson VA, Walker BD;

XX WPI; 1990-007302/01.

XX N-PSDB; AAQ03006.

XX Combinations of soluble T4 protein and anti-retro-viral agent - having

XX synergistic activity in treatment and prevention of AIDS, arc and HIV

XX infection.

XX Disclosure; Fig 2; 100pp; English.

XX X = stop codon. The sequence was deduced from the cDNA insert of PBG183.

XX Soluble T4 constructs may be produced by truncating this sequence to give

XX fragments from position 400 to 799, removing the transmembrane and

XX intracytoplasmic domains whilst retaining the extracellular region

XX responsible for HIV binding. The sol. T4 is combined with an anti-viral

XX agent such as AZT. See also AAQ03005. (Updated on 31-OCT-2002 to add

XX missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 2037 AA;

XX

Query Match 78.1%; Score 1029; DB 2; Length 2037;

Best Local Similarity 100.0%; Pred. No. 9.7e-63;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

DB 403 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 462

QY 61 ILGNQGSFLTKGPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEQKEEVOL 120

DB 463 ILGNQGSFLTKGPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEQKEEVOL 522

QY 121 LVFGLTANSDDTHLLOGOSLTLLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180

DB 523 LVFGLTANSDDTHLLOGOSLTLLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 582

QY 181 TWTCVTLQNKVKVEFKIDIV 200
 |||||
 DB 583 TWTCVTLQNKVKVEFKIDIV 602

RESULT 49

AA07641
 ID AAR07641 standard; protein; 2050 AA.

XX AAR07641;

XX 31-OCT-2002 (revised)

XX 20-DEC-1990 (first entry)

XX Deduced sequence of PBG381 comprising truncated T4 glycoprotein.

XX plasmid PBG381; soluble T4 protein; AIDS; ARC; HIV.

XX Synthetic.

XX Key Location/Qualifiers

XX Protein 403..803

XX WO9008198-A.

XX 26-JUL-1990.

XX 18-JAN-1989; 89US-00300096.

XX 18-JAN-1989; 89US-00300096.

XX (HARD) HARVARD COLLEGE.

XX Letvin NA;

XX WPI; 1990-254040/33.

XX N-PSDB; AAQ05608.

XX Treating or preventing AIDS, ARC or HIV infection - by administering an

XX immunologically effective amt. of soluble T4 protein.

XX Disclosure; Fig 2; 121pp; English.

XX Entire sequence translation of plasmid PBG381 used to transform Chinese

XX Hamster Ovary cells for the production of soluble truncated T4.

XX Transmembrane and cytoplasmic domain-encoding regions are deleted from

XX the T4 CDS to encode a truncated protein. The soluble forms may be

XX modified to increase their immunogenicity by addition of an adjuvant such

XX as incomplete Freund's adjuvant. The T4 interferes with HIV/T4

XX interaction and elicits anti-soluble T4 antibody prodn. See also

XX AAQ05607. (Updated on 31-OCT-2002 to add missing OS field.)

XX Sequence 2050 AA;

XX

Query Match 78.1%; Score 1029; DB 2; Length 2050;

Best Local Similarity 100.0%; Pred. No. 9.8e-63;

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 60

DB 403 MNRGVPFRHLILVQLALIPATQGNKVVLGKKGDTVELTCTASOKKSIQFHKNSNOIK 462

QY 61 ILGNQGSFLTKGPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEQKEEVOL 120

DB 463 ILGNQGSFLTKGPKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEQKEEVOL 522

QY 121 LVFGLTANSDDTHLLOGOSLTLLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180

DB 523 LVFGLTANSDDTHLLOGOSLTLLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 582

QY 181 TWTCVTLQNKVKVEFKIDIV 200

Db 583 TWTCVLOKQKVEFKIDIV 602

RESULT 50
AAR26532
ID AAR26532 standard; protein; 310 AA.
XX
AC AAR26532;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX
DE Sequence of CD4-kappa chimeric light chain heterotetramer.
XX
KM CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;
KM therapy; diagnostic agent; inhibition.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..204
FT /label= CD4
FT /note= "1..25 = preregion"
FT 205..310
FT /label= C kappa
XX
PN WO9213559-A1.
XX
XX 20-AUG-1992.
XX
XX 10-FEB-1992; 92WO-US001152.
XX
PR 08-FEB-1991; 91US-00654205.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
PI Beadry GA, Maddon PJ;
XX
XX WPI; 1992-299758/36.
XX
DR N-PSDB; AA027832.
XX
XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT for preventing and treating HIV infection useful as a diagnostic agent.
XX
XX Example; Fig 5; 88pp; English.
XX
XX The human kappa light chain constant region is excised from the plasmid
CC pCkappa light and ligated to M13mp18. The purified vector containing the
CC kappa light chain constant region is then ligated to human CD4 cDNA. The
CC cDNA is used to prepare an expression vector encoding the light chains of
CC a CD4-IgG1 chimeric heterotetramer designated CD4-KLC-prcCMV (ATCC
CC 75194). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 310 AA;

Query Match 78.0%; Score 1027; DB 2; Length 310;
Best Local Similarity 84.8%; Pred. No. 1.6e-63;
Matches 207; Conservative 4; Mismatches 21; Indels 12; Gaps 1;

QY 1 MNRGVPRLHLVQLALPAATQGNKVLGKGDVETLCTASQKSIQPHWNSNQIK 60
DB 1 MNRGVPRLHLVQLALPAATQGNKVLGKGDVETLCTASQKSIQPHWNSNQIK 60
QY 61 ILNGQSFLLTKGPKLNDRADSRSLWDQGNFLLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILNGQSFLLTKGPKLNDRADSRSLWDQGNFLLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFELTNSDTHLLOQSLTTLSPGSSPSVOCRSBRGNITOGGTLVSQLELDGSG 180
DB 121 LVFELTNSDTHLLOQSLTTLSPGSSPSVOCRSBRGNITOGGTLVSQLELDGSG 180
QY 181 TWTCVLOKQKVEFKIDIVRASALPAPPTGALPDPQTASALPDPPAASALPALAVI 240
DB 181 TWTCVLOKQKVEFKIDIVRASALPAPPTGALPDPQTASALPDPPAASALPALAVI 240

Db 181 TWTCVLOKQKVEFKIDIVIAFTVAAP-----SVFIPEPSDEQLKSGTASV 228

QY 241 SFLL 244
DB 229 VCUL 232

RESULT 51
AAR46679
ID AAR46679 standard; protein; 530 AA.
XX
AC AAR46679;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1994 (first entry)
XX
XX CD4-IgG2 chimeric heavy chain.
XX
XX CD4; gamma; heavy chain; chimeric; chimeric; immunconjugate; HIV;
KM human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
KM imaging; detection; targeting; immunoglobulin; IgG.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..204
FT /label= CD4 Region.
FT Region 205..302
FT /label= CH1 Region.
FT Region 303..314
FT /label= Hinge Region.
FT Region 315..423
FT /label= CH2 Region.
FT Region 424..530
FT /label= CH3 Region.
XX
XX WO9403191-A1.
XX
XX 17-FEB-1994.
XX
XX 06-AUG-1993; 93WO-US007422.
XX
XX 07-AUG-1992; 92US-00927931.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
PI Allaway GP, Maddon PJ;
XX
XX WPI; 1994-065392/08.
XX
DR N-PSDB; AA055751.
XX
XX Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2
PT immunoconjugates - used to kill HIV-infected cells and to image and
PT stage HIV infection.
XX
XX Disclosure; Fig 4; 142pp; English.
XX
XX A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy
CC chains and two kappa light chains or CD4-kappa light chains (AAR46680)
CC linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide
CC of low to moderate cytotoxicity. The resulting immunoconjugate comprising
CC the toxin can be used to kill HIV infected cells and to treat HIV
CC infected subjects to reduce the population of HIV infected cells. It can
CC also be used to reduce the likelihood of infection. The immunoconjugate
CC comprising the radionuclide can be used to image HIV infected tissue, to
CC calculate the stage of HIV infection or the efficacy of an anti-HIV
CC treatment using the imaging technique and for determining the prognosis
CC of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 530 AA;

Query Match 77.9%; Score 1026.5; DB 2; Length 530;
Best Local Similarity 84.4%; Pred. No. 3.2e-63;

Matches 206; Conservative 6; Mismatches 21; Indels 11; Gaps 1;
QY 1 MNRGVPFRHLVLTALIPATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNQIK 60
DB 1 MNRGVPFRHLVLTALIPATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNQIK 60
QY 61 ILGNQGSFLTCKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYVL 120
DB 61 ILGNRGSFLTCKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYVL 120
QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
QY 181 TWTCTVLQGNOKKVEPKIDIVPASAALPAPTGSALPDPTASALPPPPASALPALAVI 240
DB 181 TWTCTVLQGNOKKVEPKIDIVVLAFAATKGP-----SVFPLAFCRSITSESTAAI 229
QY 241 SFPL 244
DB 230 GCLV 233
RESULT 52
AAP93506
ID AAP93506 standard; protein; 394 AA.
XX AAP93506;
AC AAP93506;
DT 25-MAR-2003 (revised)
DT 02-JUN-1990 (first entry)
XX
XX
DE Derived sequence of soluble T4 lymphocyte surface protein (sT4).
KM Soluble T4 lymphocyte surface protein; sT4; AIDS therapy; AIDS diagnosis.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Protein 26..394
FT Misc-difference 26..26
FT /note= "When sequence was determined by amino acid
FT sequencing, this residue was Lys." 27..45
FT Region /note= "These residues are identical to those determined
FT by amino acid sequencing"
XX
XX EPJ13377-A.
XX
XX
XX 26-APR-1989.
XX
XX 21-OCT-1988; 88EP-00309907.
XX
XX 23-OCT-1987; 87US-00112800.
XX
XX (SMIK) SMITHKLINE BECKMAN CORP.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX PI Deen KC, Folenawaas GM, Inacker RH, Sweet RW;
XX
XX WPI; 1989-124209/17.
XX N-PSDB; AAN90763.
XX
XX Purifying soluble recombinant T4 lymphocyte surface protein - from cell
XX culture by adsorption on cation exchanger, elution and treatment with
XX anion exchanger.
XX
XX Disclosure; Fig 1; 13pp; English.
XX
XX The coding sequence is derived from the published sequence of sT4. sT4 is
XX useful in the prevention and treatment of AIDS by inhibiting spread of
XX the virus. It can also be used as an inhibitor of T4+ cell function, as a
XX reagent for identifying inhibitors of T4+ cell interaction and to produce

CC diagnostic monoclonal antibodies. (updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX
SO Sequence 394 AA;
Query Match 77.9%; Score 1026; DB 1; Length 394;
Best Local Similarity 99.5%; Pred. No. 2,5e-63;
Matches 199; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLVLTALIPATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNQIK 60
DB 1 MNRGVPFRHLVLTALIPATQGNKVLTGKKGDTVELTCTASOKKSTIOFHKNSNQIK 60
QY 61 ILGNQGSFLTCKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYVL 120
DB 61 ILGNQGSFLTCKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYVL 120
QY 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
DB 121 LVFGLTANSPTHTLQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLEIQDSG 180
QY 181 TWTCTVLQGNOKKVEPKIDIV 200
DB 181 TWTCTVLQGNOKKVEPKIDIV 200
RESULT 53
AAE37197
ID AAE37197 standard; protein; 202 AA.
XX AAE37197;
AC AAE37197;
XX
XX
DT 07-AUG-2003 (first entry)
XX
XX
DE sCD4 protein.
XX
XX CD4-inducible epitope; Human immunodeficiency virus; HIV; gene therapy;
XX HIV infection; envelope glycoprotein; Env; vaccine; sCD4.
XX
XX Unidentified.
XX
XX WO2003033666-A2.
XX
XX 24-APR-2003.
XX
XX 16-OCT-2002; 2002WO-US033165.
XX
XX 16-OCT-2001; 2001US-0329709P.
XX
XX (SCRI) SCRIPPS RES INST.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Dimitrov DS, Moulard M, Xiao X, Shu Y, Phogat SK, Zhang M;
XX Burton D;
XX
XX WPI; 2003-393518/37.
XX
XX
XX New isolated antibody or antibody fragment specifically binds a CD4-
XX inducible epitope on Human Immunodeficiency Virus (HIV) Env proteins,
XX useful for preparing a composition for treating or preventing HIV
XX infection.
XX
XX Example 3; Page 33; 69pp; English.
XX
XX The invention relates to antibodies or antibody fragments specifically
XX binding to CD4-inducible epitope on Human immunodeficiency virus (HIV)
XX envelope glycoprotein (Env) proteins. The antibody is useful for
XX preparing a composition for treating or preventing HIV infection. The
XX invention is used to prepare vaccines and is used in gene therapy. The
XX present sequence is a sCD4 protein used in the exemplification of the
XX invention
XX
XX Sequence 202 AA;


```
Query Match          77.7%; Score 1023; DB 6; Length 202;
Best Local Similarity 99.5%; Pred. No. 1.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRRHLLVLTQLALPPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
DB 1 MNRGVPPRRHLLVLTQLALPPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 54
AAR07605
ID AAR07605 standard; protein; 295 AA.
XX
AC AAR07605;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 06-FEB-1991 (first entry)
XX
DE Plasmid T4/LFA-3/AD gene product with C-terminal encoding
DE phosphatidylinositol (PI) linkage signaling sequence.
XX
KM Plasma membrane binding affinity; micelle.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Protein 1..266
FT /label= T4/LFA-3/AD gene product
FT Peptide 267..295
FT /label= PI signal peptide
XX
PN W09012099-A.
XX
PD 18-OCT-1990.
XX
PF 10-APR-1989; 89US-00335688.
XX
PR 10-APR-1989; 89US-00335688.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Wallner BP;
XX
DR WPI; 1990-334849/44.
DR N-PSDB; AAQ06404.
XX
PT Phosphatidyl-inositol linkage signalling DNA sequence - derived from
PT lymphocyte function-associated antigen 3, used for prodn. of chimeric
PT proteins.
XX
PS Disclosure; Fig 4; 53pp; English.
XX
CC The signal sequence is attached downstream of the plasmid sequence
CC encoding a secreted protein, which will then produce proteins covalently
CC anchored to the cell surface in which they were produced. This can give
CC rise to plasma membrane binding, enhanced purifiability, micelle
CC formation etc. especially useful in the production of chimeric targeted
CC drugs, to produce micellar or liposomal delivery systems or in enhanced
CC purification and screening of cells, proteins or DNA libraries. (Updated
```

```
CC on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 295 AA;
Query Match          77.7%; Score 1023; DB 2; Length 295;
Best Local Similarity 99.5%; Pred. No. 3e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRRHLLVLTQLALPPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
DB 1 MNRGVPPRRHLLVLTQLALPPAATQGNKVVLGKKGDVVELTCTASQKKSIOFHWKNSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 55
AAR07606
ID AAR07606 standard; protein; 318 AA.
XX
AC AAR07606;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 06-FEB-1991 (first entry)
XX
DE Plasmid T4/LFA-3/2 gene product with C-terminal encoding
DE phosphatidylinositol (PI) linkage signaling sequence.
XX
KM Plasma membrane binding affinity; micelle.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Protein 1..267
FT /label= LFA-3 gene product
FT Peptide 267..318
FT /label= PI signal peptide
XX
PN W09012099-A.
XX
PD 18-OCT-1990.
XX
PF 10-APR-1989; 89US-00335688.
XX
PR 10-APR-1989; 89US-00335688.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Wallner BP;
XX
DR WPI; 1990-334849/44.
DR N-PSDB; AAQ06405.
XX
PT Phosphatidyl-inositol linkage signalling DNA sequence - derived from
PT lymphocyte function-associated antigen 3, used for prodn. of chimeric
PT proteins.
XX
PS Disclosure; Fig 5; 53pp; English.
XX
CC The signal sequence is attached downstream of the plasmid sequence
CC encoding a secreted protein, which will then produce proteins covalently
CC anchored to the cell surface in which they were produced. This can give
```

CC rise to plasma membrane binding, enhanced purifiability, micelle
 CC formation etc. especially useful in the production of chimeric targeted
 CC drugs, to produce micellar or liposomal delivery systems or in enhanced
 CC purification and screening of cells, proteins or DNA libraries. (Updated
 CC on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)

XX Sequence 318 AA;

Query Match 77.7%; Score 1023; DB 2; Length 318;

Best Local Similarity 99.5%; Pred. No. 3.2e-63; Indels 0; Gaps 0;

Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPATQGNKVLGKKGDVLTCTASQKSIQFHMKNNOIK 60
 Db 1 MNRGVPRHLLVLTQALLPATQGNKVLGKKGDVLTCTASQKSIQFHMKNNOIK 60
 QY 61 ILGNQGSFLTGPSPKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVL 120
 Db 61 ILGNQGSFLTGPSPKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVL 120
 QY 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 Db 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKVKVEFKIDIV 200
 Db 181 TWTCTVLQNKVKVEFKIDIV 200

RESULT 56

AAV39825
 ID AAV39825 standard; protein; 394 AA.

XX AAV39825;

XX 03-DEC-1999 (first entry)

XX Soluble human T4 protein.

XX Soluble T4 protein; sT4; human; HIV; binding inhibitor; T4+ cell; AIDS;

XX vaccine; immunisation; therapy.

XX Homo sapiens.

XX US5958678-A.

XX 28-SEP-1999.

XX 12-DEC-1994; 94US-00354452.

XX 21-AUG-1986; 86US-00898587.

XX 11-JUN-1991; 92US-00713564.

XX 06-JUL-1992; 92US-00909021.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Mcdougal JS, Weiss R, Axel R, Littman DR, Maddon PJ, Chess L,

XX WPI; 1999-561025/47.

XX N-PSDB; AA220694.

XX Human T4 protein inhibits HIV binding to T4 cells, useful for treating

XX AIDS.

XX Disclosure; Col 13-16; 58pp; English.

XX This sequence represents the soluble human T4 protein of the invention.
 CC The soluble human T4 protein blocks the binding of HIV to T4+ cells and
 CC is therefore useful for the treatment of AIDS. Monoclonal antibodies
 CC against the T4 protein may be used as vaccines for immunising subjects
 CC against AIDS
 XX

SQ Sequence 394 AA;

Query Match 77.7%; Score 1023; DB 2; Length 394;

Best Local Similarity 99.5%; Pred. No. 4.1e-63; Indels 0; Gaps 0;

Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPATQGNKVLGKKGDVLTCTASQKSIQFHMKNNOIK 60
 Db 1 MNRGVPRHLLVLTQALLPATQGNKVLGKKGDVLTCTASQKSIQFHMKNNOIK 60
 QY 61 ILGNQGSFLTGPSPKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVL 120
 Db 61 ILGNQGSFLTGPSPKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVDQKEEVL 120
 QY 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 Db 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKVKVEFKIDIV 200
 Db 181 TWTCTVLQNKVKVEFKIDIV 200

RESULT 57

AAV88328
 ID AAV88328 standard; protein; 394 AA.

XX AAV88328;

XX 14-JUL-2000 (first entry)

XX T4 glycoprotein amino acid sequence.

XX sT4; glycoprotein; human immunodeficiency virus; HIV; block binding;

XX AIDS; treatment; inhibic; cell to cell spread; infection; fusion.

XX Mammalia.

XX US5126433-A.

XX 30-JUN-1992.

XX 23-OCT-1987; 87US-00114244.

XX 21-AUG-1986; 86US-00898587.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Maddon PJ, Chess L, Weiss R, Littman DR, Mcdougal JS;

XX WPI; 2000-348913/30.

XX N-PSDB; AAA10906.

XX Soluble T4 glycoprotein useful for prevention and treatment of acquired

XX immunodeficiency syndrome and for screening inhibitors of human

XX immunodeficiency viral binding.

XX Disclosure; Col 11-16; 64pp; English.

XX This sequence represents the full length amino acid sequence of

XX glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses

XX sT4 as a target receptor on T cells. The invention relates to

XX glycosylated sT4 which functions by blocking the binding of HIV to T4

XX target cells, and can be used for the prophylaxis and treatment of AIDS

XX patients. Administration of sT4 effectively inhibits the cell to cell
 CC spreading of HIV infection and also the fusion of HIV-infected T4 cells
 CC and non-infected T4 cells. The administration of T4 alleviates several
 CC symptoms associated with AIDS. The occurrence of new
 CC pathological changes. The sT4 glycoprotein is useful for the prophylaxis
 CC and treatment of patients with AIDS. It is also useful as a reagent to
 CC identify natural, synthetic or recombinant molecules which act as
 CC therapeutic agents or inhibitors of T4 cell interactions and in
 CC diagnostic assays for detection T4 proteins or molecules

XX Sequence 394 AA;
 SQ Query Match 77.7%; Score 1023; DB 3; Length 394;
 Best Local Similarity 99.5%; Pred. No. 4.1e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQIK 60
 Db 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQIK 60

61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIINKLIKIEDSDTYICEVEDQKEEVL 120
 Db 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIINKLIKIEDSDTYICEVEDQKEEVL 120

121 LVFGLTANS DTHLQGSILTLTLESPPGSSPSVQCSPKGNIOGKTLISVSQLELDQSG 180
 Db 121 LVFGLTANS DTHLQGSILTLTLESPPGSSPSVQCSPKGNIOGKTLISVSQLELDQSG 180

181 TWCTVLOKQKVEFKIDIV 200
 Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 58
 AAB19509
 ID AAB19509 standard; protein; 416 AA.
 XX
 AC AAB19509;
 XX
 DT 09-JAN-2001 (first entry)
 XX
 DE CD4-IgM fusion protein CH4Mmu.
 XX
 KM CD4; IgM; human; CD4Mmu; fusion protein; immunoglobulin; HIV; SIV; gp120;
 KM therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..395
 FT /note= "CD4 extracellular region"
 FT Protein 400..416
 FT /note= "IgM heavy chain partial sequence"
 XX
 PN US6117656-A.
 XX
 XX 12-SEP-2000.
 XX
 PF 07-JUN-1995; 95US-00479353.
 XX
 XX 22-JAN-1988; 88US-00147351.
 XX 23-JAN-1989; 89US-00299596.
 XX 09-JUN-1992; 92US-00896781.
 XX 12-APR-1993; 93US-00057952.
 XX 04-FEB-1994; 94US-00191708.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX
 XX Seed B;
 XX
 DR WPI; 2000-586558/55.
 DR N-PSDB; AAA50662.
 XX
 PT CD4-Immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
 PT SIV.
 XX
 PS Example 1; Col 41-50; 39pp; English.
 XX
 CC The present sequence is that of fusion protein CD4Mmu comprising the
 CC extracellular portion of CD4, which binds to HIV gp120, linked at its C-
 CC terminus to the human IgM heavy chain. To obtain the fusion protein, DNA
 CC encoding CD4 was linked to IgM DNA at the NotI site upstream of the CH1

CC region (see AAA50662). Fusion protein CD4Mmu and a nucleic acid encoding
 CC it are claimed. Also claimed are a vector comprising the nucleic acid,
 CC and a method of producing the fusion protein in secreted form using a
 CC transformed host cell. The fusion protein may further comprise a
 CC therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
 CC can be administered to an animal (including humans) for treatment of HIV
 CC or SIV infection, and can also be used in assays for HIV or SIV, imaging
 CC and tissue stains. IgM fusion proteins such as CD4Mmu provide complement-
 CC mediated immunity
 XX
 SQ Sequence 416 AA;
 Query Match 77.7%; Score 1023; DB 3; Length 416;
 Best Local Similarity 99.5%; Pred. No. 4.3e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQIK 60
 Db 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQIK 60

61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIINKLIKIEDSDTYICEVEDQKEEVL 120
 Db 61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIINKLIKIEDSDTYICEVEDQKEEVL 120

121 LVFGLTANS DTHLQGSILTLTLESPPGSSPSVQCSPKGNIOGKTLISVSQLELDQSG 180
 Db 121 LVFGLTANS DTHLQGSILTLTLESPPGSSPSVQCSPKGNIOGKTLISVSQLELDQSG 180

181 TWCTVLOKQKVEFKIDIV 200
 Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 59
 AAAY51080
 ID AAAY51080 standard; protein; 436 AA.
 XX
 AC AAAY51080;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human fusion protein CD4Mg.
 XX
 KM Fusion protein; human; CD4; IgM; immunoglobulin; gp120;
 KM anti-human immunodeficiency virus; CD4Mg.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US6004761-A.
 XX
 XX 21-DEC-1999.
 XX
 PF 04-FEB-1994; 94US-00191708.
 XX
 XX 22-JAN-1988; 88US-00147351.
 XX 23-JAN-1989; 89US-00299596.
 XX 09-JUN-1992; 92US-00896781.
 XX 12-APR-1993; 93US-00057952.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 XX
 XX Seed B;
 XX
 DR WPI; 2000-085792/07.
 DR N-PSDB; AA244063.
 XX
 PT Fusion protein useful for the treatment of human immunodeficiency virus.
 PT
 XX
 PS Example 1; Col 41-50; 39pp; English.
 XX
 CC This invention describes a novel nucleic acid (I) encoding a fusion
 CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)

CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC chain (II). The products of the invention have anti-human
CC immunodeficiency virus (HIV) activity and are capable of binding to
CC gp120. The fusion protein is useful for treating human immunodeficiency
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC represents the fusion protein CD4mg which is constructed from CD4 linked
CC to human Igm upstream of the CH1 region

SQ Sequence 436 AA;

Query Match	77.7%;	Score 1023;	DB 3;	Length 436;
Best Local Similarity	99.5%;	Pred. No. 4.6e-63;		
Matches 199; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

Qy	1	MNGVPRRHLLVLQALALPAATQGGKVVLGKKGTVELCTASQKSIQPHMNSQIK	60
Db	1	MNGVPRRHLLVLQALLPAATQGGKVVLGKKGTVELCTASQKSIQPHMNSQIK	60
Qy	61	ILNQGSPFLTKGSPSKLNDRAISRSLMDQGNFLLIKNLKIEDSPVYICEVEDQKEVOL	120
Db	61	ILNQGSPFLTKGSKLNDRAISRSLMDQGNFLLIKNLKIEDSPVYICEVEDQKEVOL	120
Qy	121	LVFGLTANSDPTHLLQGQSILTLTLESPGSSPSVQGRSPRGKNIQGGKTLVSQLELDQSG	180
Db	121	LVFGLTANSDPTHLLQGQSILTLTLESPGSSPSVQGRSPRGKNIQGGKTLVSQLELDQSG	180
Qy	181	TWTCTVLAQNKVKEFKIDIV	200
Db	181	TWTCTVLAQNKVKEFKIDIV	200

RESULT 60
AAV88329
ID AAV88329 standard; protein; 458 AA

AC	AAV88329;	
XX		
DT	14-JUL-2000	(first entry)
XX		
DE	T4 glycoprotein amino acid sequence	

KM 874; glycoprotein; human immunodeficiency virus; HIV; block binding
 KM AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
 XX
 XX Mammalia.
 OS
 XX
 PN US5126433-A.
 XX
 PD 30-JUN-1992.
 XX
 PF 23-OCT-1987; 87US-00114244.
 XX
 ER 21-AUG-1986; 86US-00898587.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK

PI	Maddon PJ, Chess L, Axel R, Weiss R, Littman DR, McDougal JS,
XX	
DR	WPI; 2000-348913/30.

PT Soluble T4 glycoprotein useful for prevention and treatment of acquired
PT immunodeficiency syndrome and for screening inhibitors of human
PT immunodeficiency viral binding.

PS Example; Fig 6; 64pp; English.

CC This sentence represents the amino acid sequence of glycosylated srt4
CC glycoprotein. Human immunodeficiency virus (HIV) uses srt4 as a target
CC receptor on T cells. The invention relates to glycosylated srt4 which
CC functions by blocking the binding of HIV to T4 target cells, and can be
CC used for the prophylaxis and treatment of AIDS patients. Administration
CC of srt4 effectively inhibits the cell to cell spreading of HIV infection
CC and also the fusion of HIV-infected T4 cells and non-infected T4 cells

The administration of T4 alleviates several symptoms associated with AIDS and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful for the prophylaxis and treatment of patients with AIDS. It is also useful as a reagent to identify natural, synthetic or recombinant molecules which act as therapeutic agents or inhibitors of T4 cell interactions and in diagnostic assays for detection T4 proteins or molecules

SQ Sequence 458 AA;

Query Match	77.7%	Score 1023	DB 3	Length 458
Best Local Similarity	99.5%	Pred. No. 4.8e-63		
Matches 199	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy	1	MNRGVEFRHLHLVLOLALLPATQGNKVVLGGKGYEALTCTAQQKSIQPHMKNNOIK	60
Db	1	MNRGVEFRHLHLVLOLALLPATQGNKVVLGGKGYEALTCTAQQKSIQPHMKNNOIK	60
Qy	61	ILNQGSSFLTKGSPSKLNRADSRRLSDMQGNFPLIKLKIEDSDTYICEVEDQKEVOL	120
Db	61	ILNQGSSFLTKGSPSKLNRADSRRLSDMQGNFPLIKLKIEDSDTYICEVEDQKEVOL	120
Qy	121	LVFGLTANSDBTHLLOQOSITLTLESPPGSSPSVQCRSPRGKNIQGGKITLSVSOLELDSG	180
Db	121	LVFGLTANSDBTHLLOQOSITLTLESPPGSSPSVQCRSPRGKNIQGGKITLSVSOLELDSG	180
Qy	181	TWTCYVLQNOQKVEFKIDIV	200
Db	181	TWTCYVLQNOQKVEFKIDIV	200

RESULT 61
AAB81502
ID AAB81502 standard; protein; 458 AA

AC	AAB81502;
XX	
DT	18-JUN-2001 (first entry)
XX	
DE	Human CD4 protein.

KW Human; CD4 fusion protein; oligomerization;
 KW receptor-ligand interaction; inhibition; surface plasmon resonance; SPR;
 KW T cell receptor binding; MHC binding; carcinoma; autoimmune disease;
 KW multiple sclerosis; human immunodeficiency virus; HIV; diabetes;
 KW rheumatoid arthritis; immune disorder.

OS Homo sapiens.

EH	Key	Location/Qualifiers
PT	Peptide	1..25
PT		/label=Signal_peptide
PT	Protein	26..458
PT		/label=Human_CD4

PN WO200122084-A2.

PD 29-MAR-2001

PF 18-SEP-2000; 2000WO-GB003579

PR 21-SEP-1999; 99GB-00022352.

PA (AVID-) AVIDEX LTD

PI Jakobsen BK

DR WPI; 2001-273470/28
DR N-PSDB; AAF82582.

PT Sequential screening of candidate compounds library for those which inhibit binding of low affinity receptor-ligand interaction having fast binding kinetics, using interfacial optical assay.

XX PS Disclosure; Fig 13; 91pp; English.

CC XX The present sequence is human CD4. Human CD4 extracellular domains 1 and 2 were used in the construction of CD4 oligomerisation fusion proteins. The fusion proteins contain an oligomerisation domain that enables the proteins to bind to one another to form oligomers. The oligomers may be used in an invention relating to a method for screening for compounds with the ability to inhibit a low affinity receptor-ligand interaction. The method uses an interfacial optical assay, such as surface plasmon resonance (SPR). The method is useful for screening candidate compounds for the ability to inhibit interaction between MHC/peptide complex and T cell receptor, and MHC/peptide complex and CD8 or CD4 co-receptor. The compound identified by the above methods which interfere with T cell receptor binding to a particular HLA type molecule are useful as immune inhibitors for treating carcinomas, autoimmune diseases such as multiple sclerosis, human immunodeficiency virus (HIV) infection, rheumatoid arthritis, Hashimoto's disease, insulin dependent diabetes, Good pasture's syndrome, uveitis, psoriasis and graft rejection

CC XX

CC SQ Sequence 458 AA;

Query Match 77.7%; Score 1023; DB 4; Length 458;
Best Local Similarity 99.5%; Pred. No. 4.8e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAQGNKVVLGKGGDTVELTCTASOKKSIOFHKNSNOIK 60
DB 1 MNRGVPRHLLLVQLALPAAQGNKVVLGKGGDTVELTCTASOKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSPTHLLOQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVLOQNKKEFKIDIV 200
DB 181 TWTCVLOQNKKEFKIDIV 200

RESULT 62
AAG79087
ID AAG79087 standard; protein; 458 AA.
XX
AC AAG79087;
XX
DT 10-DEC-2001 (first entry)
XX
DE Amino acid sequence of human CD4 protein.
XX
KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CD4.
XX
OS Homo sapiens.
XX
PN MO200164752-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006322.
XX
PR 02-MAR-2000; 2000US-00517605.
XX
PA (UNYNY) UNIV NEW YORK STATE.
XX
PA (UNYNY -) UNIV NIJMEGEN.
XX
PI Litman DR, Kwon D, Van Kooyk Y, Geljtenbeek T;
XX
DR WPI; 2001-602565/68.
XX

PT An antibody for the treatment or prevention of HIV-infection comprises a gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of PT DC-SIGN due to concomitant conformational change.

CC XX

CC PS Disclosure; Page 115-116; 131pp; English.

CC XX The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CD4 protein

CC XX

CC SQ Sequence 458 AA;

Query Match 77.7%; Score 1023; DB 4; Length 458;
Best Local Similarity 99.5%; Pred. No. 4.8e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAQGNKVVLGKGGDTVELTCTASOKKSIOFHKNSNOIK 60
DB 1 MNRGVPRHLLLVQLALPAAQGNKVVLGKGGDTVELTCTASOKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIKNLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSPTHLLOQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVLOQNKKEFKIDIV 200
DB 181 TWTCVLOQNKKEFKIDIV 200

RESULT 63
ADD25609
ID ADD25609 standard; protein; 458 AA.
XX
AC ADD25609;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated protein #82.
XX
KW Binding domain; immunoglobulin; fusion protein; cytosolic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
XX
XX US2003118592-A1.
XX
XX
XX 26-JUN-2003.
XX
XX
XX 25-JUL-2002; 2002US-00207655.
XX
XX
XX 17-JAN-2001; 2001US-0367358P.
XX
XX 17-JAN-2002; 2002US-00053530.
XX
XX 03-JUN-2002; 2002US-0385691P.
XX
XX (GENE-) GENE-CRAFT INC.
XX

XX Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
PI WPI; 2003-801317/75.
XX
XX New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
XX Disclosure; SEQ ID NO 170; 157pp; English.
XX
XX The invention relates to a binding domain-immunoglobulin fusion protein
CC comprising a binding domain polypeptide that is fused to an
CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC CH2 constant region polypeptide that is fused to the hinge region
CC polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC polypeptide that is fused to the CH2 constant region polypeptide. The
CC hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC region polypeptide, derived from (a) having 3 or more cysteine residues;
CC where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC contains 2 cysteine residues, where the first cysteine is not mutated; a
CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC (a) having 3 or more cysteine residues, where the mutated human IgG1
CC immunoglobulin hinge region polypeptide contains no more than one
CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC polypeptide, derived from (a) having 3 or more cysteine residues; where
CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC capable of at least one immunological activity comprising antibody
CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC binding domain polypeptide is capable of specifically binding to an
CC antigen. Also included are an isolated polynucleotide encoding the
CC binding domain-immunoglobulin fusion protein, a recombinant expression
CC construct comprising the polynucleotide (operably linked to a promoter),
CC a host cell transformed or transfected with a recombinant expression
CC construct, producing the binding domain-immunoglobulin fusion protein, a
CC pharmaceutical composition comprising the binding domain-immunoglobulin
CC fusion protein or polynucleotide and a carrier, and treating a subject
CC having or suspected of having a malignant condition or a B-cell disorder.
CC The binding domain-immunoglobulin fusion protein is useful for treating a
CC subject having or suspected of having a malignant condition or a B-cell
CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC sclerosis or autoimmune disease. The present sequence is a binding domain
CC -immunoglobulin fusion protein-associated protein sequence. Note: The
CC sequence data for this patent formed part of the printed specification
CC and is also available in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not
CC identified the sequences in the printed specification by their SEQ ID
CC number therefore none of the sequences can be explicitly identified.
XX
XX Sequence 458 AA;
SO
Query Match 77.7%; Score 1023; DB 7; Length 458;
Best Local Similarity 99.5%; Pred. No. 4.8e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MANGVPRHLLLVQLALLPAATQGNKVYGVGKGDYVELTCTASOKKSTOFHKNKSNQIK 60
DB 1 MANGVPRHLLLVQLALLPAATQGNKVYGVGKGDYVELTCTASOKKSTOFHKNKSNQIK 60
QY 1LGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLITKNLKIIESDPYICEVEQKKEVQL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLWDQGNFPLITKNLKIIESDPYICEVEQKKEVQL 120
QY 121 LVFGLTANSDTHLLQGQSLTILTESPPGSSPSVQCSPRGKNIQGGKTTLSVSLQLEIDQSG 180
DB 121 LVFGLTANSDTHLLQGQSLTILTESPPGSSPSVQCSPRGKNIQGGKTTLSVSLQLEIDQSG 180
QY 181 TWTCVTYQNGKVKVEFKIDIV 200
DB 181 TWTCVTYQNGKVKVEFKIDIV 200

RESULT 64
ADE57489
ID ADE57489 standard; protein; 458 AA.
XX
XX ADE57489;
AC
XX
DT 29-JAN-2004 (first entry)
XX
XX Human Protein P01730, SEQ ID NO 3351.
DE
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS
XX WO2003016475-A2.
PN
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; P01730.
DR
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
PS
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 458 AA;
SO
Query Match 77.7%; Score 1023; DB 7; Length 458;
Best Local Similarity 99.5%; Pred. No. 4.8e-63;

Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MNRGVPRRHLLVLTQALLPAAATQGNKRVLGKKDPVVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPRRHLLVLTQALLPAAATQGNKRVLGKKDPVVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLTQGSGLTTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLTQGSGLTTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKVKVEFKIDIV 200
DB 181 TWCTCTVLQNKVKVEFKIDIV 200

```

RESULT 65

ADA44807
ID ADA44807 standard; protein; 473 AA.

AC ADA44807;
DT 04-DEC-2003 (first entry)

DE CD4/TCR CD3epsilon chain chimeric protein CD4epsilon15, SEQ ID NO:2.

KW HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric CD4;

KM endoplasmic reticulum; ER retention; envelope protein gp160;

KW T cell receptor CD3epsilon chain; C-terminal domain; CD4epsilon15;

KW gene therapy; human; receptor.

OS Chimeric.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

CC expression system encoding a chimeric CD4 protein. The ER-localised

CC chimeric CD4 molecule binds to the HIV-1 envelope protein gp160,

CC resulting in HIV-1 retention in the ER and thereby preventing viral

CC replication. In a specific embodiment, the chimeric CD4 molecule

CC comprises CD4 fused to 15 amino acids of the C-terminal domain of the T

CC cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated

CC CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but

CC containing only 10 amino acids from CD3epsilon can also be used.

CC Compositions of the invention have an in trans effect on the replication

CC of HIV-1, and may be used to treat and prevent HIV-1 infection. The

CC present sequence represents the chimeric CD4 molecule CD4epsilon15, which

CC is specifically claimed for use in compositions of the invention.

XX Sequence 473 AA.

Query Match 77.7%; Score 1023; DB 7; Length 473;
Best Local Similarity 99.5%; Pred. No. 5e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MNRGVPRRHLLVLTQALLPAAATQGNKRVLGKKDPVVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPRRHLLVLTQALLPAAATQGNKRVLGKKDPVVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLTQGSGLTTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLTQGSGLTTLTLESPGSSPVQCRSPRGKNIQSGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQNKVKVEFKIDIV 200
DB 181 TWCTCTVLQNKVKVEFKIDIV 200

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RESULT 66

AA59170
ID AA59170 standard; protein; 474 AA.

AC AA59170;

DT 14-MAR-2000 (first entry)

DE CD4-Ig fusion protein CD4mu.

KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;

KW secreted protein; SIV infection; medicament.

OS Synthetic.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

The invention provides a fusion gene encoding a fusion protein that

Example 1; Page 47-53; 89pp; English.

New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in

the treatment of HIV or simian immunodeficiency virus infections.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

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Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

Example 1; Page 47-53; 89pp; English.

CC comprises an extracellular CD4 DNA sequence or its fragment which binds
 CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
 CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
 CC the variable region has been replaced with the DNA sequence which encodes
 CC extracellular CD4 or its gp120 binding fragment. The fusion protein is
 CC capable of being secreted. The fusion proteins are useful for treating
 CC HIV or SIV infections in animals, preferably humans. They are also useful
 CC for producing medicaments which can be used for treating HIV or SIV
 CC infections in humans. The present sequence represents the fusion protein
 CC CD4muu where the CD4 is linked to human IgG1 at the Met2 site upstream of
 CC the CH1 region

XX SQ Sequence 474 AA;

Query Match 77.7%; Score 1023; DB 3; Length 474;
 Best Local Similarity 99.5%; Pred. No. 5e-63; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60

QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120

QY 121 LVFGLTANSPTHTLGGOSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELODSG 180
 DB 121 LVFGLTANSPTHTLGGOSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELODSG 180

QY 181 TWTCTVLOQOKKVEFKIDIV 200
 DB 181 TWTCTVLOQOKKVEFKIDIV 200

RESULT 67
 AAB19510
 ID AAB19510 standard; protein; 481 AA.

XX AC AAB19510;
 XX DT 09-JAN-2001 (first entry)
 XX DE CD4-IgM fusion protein CH4Pmu.
 XX KM CD4; IgM; human; CD4Pmu; fusion protein; immunoglobulin; HIV; SIV; gp120;
 XX KM therapy; diagnosis.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 XX FH 1..395
 XX FT Protein /note="CD4 extracellular region"
 XX FT Protein 400..481
 XX FT /note="IgM heavy chain partial sequence"

XX PN US6117656-A.
 XX PD 12-SEP-2000.
 XX PF 07-JUN-1995; 95US-00479353.
 XX PR 22-JAN-1988; 88US-00147351.
 XX PR 23-JAN-1989; 89US-00299596.
 XX PR 09-JUN-1992; 92US-00896781.
 XX PR 12-APR-1993; 93US-00057952.
 XX PR 04-FEB-1994; 94US-00191708.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Seed B;
 XX PA WPI; 2000-586558/55.
 XX DR

DR N-PSDB; AAB50662.
 XX CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
 XX SIV.
 XX Example 1; Col 49-60; 39pp; English.

XX The present sequence is that of fusion protein CD4Pmu comprising the
 XX extracellular portion of CD4, which binds to HIV gp120, linked at its C-
 XX terminus to the human IgM heavy chain. To obtain the fusion protein, DNA
 XX encoding CD4 was linked to IgM DNA at the Pst site upstream of the CH2
 XX region (see AAB50663). Fusion protein CD4Pmu and a nucleic acid encoding
 XX it are claimed. Also claimed are a vector comprising the nucleic acid,
 XX and a method of producing the fusion protein in secreted form using a
 XX transformed host cell. The fusion protein may further comprise a
 XX therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
 XX can be administered to an animal (including humans) for treatment of HIV
 XX or SIV infection, and can also be used in assays for HIV or SIV, imaging
 XX and tissue stains. IgM fusion proteins such as CD4Pmu provide complement-
 XX mediated immunity

XX SQ Sequence 481 AA;

Query Match 77.7%; Score 1023; DB 3; Length 481;
 Best Local Similarity 99.5%; Pred. No. 5.1e-63; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLVLQALLPATQGNKVVYLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60

QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKULKIEDSDTYICEVEDQKEEYQL 120

QY 121 LVFGLTANSPTHTLGGOSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELODSG 180
 DB 121 LVFGLTANSPTHTLGGOSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELODSG 180

QY 181 TWTCTVLOQOKKVEFKIDIV 200
 DB 181 TWTCTVLOQOKKVEFKIDIV 200

RESULT 68
 AAB51081
 ID AAB51081 standard; protein; 481 AA.

XX AC AAB51081;
 XX DT 23-MAR-2000 (first entry)
 XX DE Human fusion protein CD4Pmu.
 XX KW Fusion protein; human; CD4; IgM; immunoglobulin; gp120;
 XX KW anti-human immunodeficiency virus; CD4Pmu.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US6004781-A.
 XX PD 21-DEC-1999.
 XX PF 04-FEB-1994; 94US-00191708.
 XX PR 22-JAN-1988; 88US-00147351.
 XX PR 23-JAN-1989; 89US-00299596.
 XX PR 09-JUN-1992; 92US-00896781.
 XX PR 12-APR-1993; 93US-00057952.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI
 XX PA
 XX XX

PI Seed B;
 XX WPI: 2000-095792/07.
 DR N-PSDB; AA244064.
 XX
 XX Fusion protein useful for the treatment of human immunodeficiency virus.
 PS Example 1; Col 49-58; 39pp; English.
 XX
 CC This invention describes a novel nucleic acid (I) encoding a fusion
 CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
 CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
 CC chain (III). The products of the invention have anti-human
 CC immunodeficiency virus (HIV) activity and are capable of binding to
 CC gp120. The fusion protein is useful for treating human immunodeficiency
 CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
 CC represents the fusion protein CD4pmu which is constructed from CD4 linked
 CC to human Igm upstream of the CH2 region
 XX
 SQ Sequence 481 AA;

Query Match 77.7%; Score 1023; DB 3; Length 481;
 Best Local Similarity 99.5%; Pred. No. 5.1e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQLALPPAATQGNKVYLGKGDVTELTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLVLTQLALPPAATQGNKVYLGKGDVTELTCTASQKKSIOFHKNSNOIK 60
 QY 61 ILGNQGSFLTQGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTQGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180
 DB 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180
 QY 181 TWCTCVLONOKKVEFKIDIV 200
 DB 181 TWCTCVLONOKKVEFKIDIV 200

RESULT 69
 AA59171
 ID AA59171 standard; protein; 481 AA.

XX AC AA59171;
 XX DT 14-MAR-2000 (first entry)
 XX DE CD4-Ig fusion protein CD4pmu.
 XX KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
 XX KM secreted protein; SIV infection; medicament.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN CA1340741-C.
 XX PD 14-SEP-1999.
 XX PF 20-JAN-1989; 89CA-00588749.
 XX PR 20-JAN-1989; 89CA-00588749.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Seed B;
 XX WPI: 2000-063015/06.
 XX DR N-PSDB; AA248204.

PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
 PT the treatment of HIV or simian immunodeficiency virus infections.
 XX
 XX Example 1; Page 54-60; 89pp; English.
 PS

CC The invention provides a fusion gene encoding a fusion protein that
 CC comprises an extracellular CD4 DNA sequence or its fragment which binds
 CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
 CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
 CC the variable region has been replaced with the DNA sequence which encodes
 CC extracellular CD4 or its gp120 binding fragment. The fusion protein is
 CC capable of being secreted. The fusion proteins are useful for treating
 CC HIV or SIV infections in animals, preferably humans. They are also useful
 CC for producing medicaments which can be used for treating HIV or SIV
 CC infections in humans. The present sequence represents the fusion protein
 CC CD4pmu where the CD4 is linked to human IgG1 at the Pst site upstream of
 CC the CH2 region
 XX
 SQ Sequence 481 AA;

Query Match 77.7%; Score 1023; DB 3; Length 481;
 Best Local Similarity 99.5%; Pred. No. 5.1e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQLALPPAATQGNKVYLGKGDVTELTCTASQKKSIOFHKNSNOIK 60
 DB 1 MNRGVPFRHLVLTQLALPPAATQGNKVYLGKGDVTELTCTASQKKSIOFHKNSNOIK 60
 QY 61 ILGNQGSFLTQGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTQGPSKLNDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180
 DB 121 LVFGLTANSDTHLLQGSQSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDGSG 180
 QY 181 TWCTCVLONOKKVEFKIDIV 200
 DB 181 TWCTCVLONOKKVEFKIDIV 200

RESULT 70
 AAB00158
 ID AAB00158 standard; protein; 507 AA.

XX AC AAB00158;
 XX DT 08-FEB-2001 (first entry)
 XX DE sCD4-sCFv(17b) HIV single chain antibody fusion protein.
 XX KW Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS;
 XX KM acquired immune deficiency syndrome; neutralisation; infection;
 XX KW gene therapy; CD4; gp120; glycoprotein; resistance; vaccination;
 XX binding domain; single chain antibody; chimera; chimeric protein.
 XX OS Human immunodeficiency virus.
 XX OS Synthetic.
 XX PN WO200055207-A1.
 XX PD 21-SEP-2000.
 XX PF 16-MAR-2000; 2000MO-US006946.
 XX PR 16-MAR-1999; 99US-0124681P.
 XX PA (USSH) US NAT INST OF HEALTH.
 XX PI Berger EA, Del Castillo CM;
 XX WPI: 2000-638183/61.
 XX DR N-PSDB; AA454045.

XX Novel neutralizing bispecific fusion proteins effective in viral such as
 PT HIV neutralization, comprises two different binding domains, inducing-
 PT binding domain and induced-binding domain functionally linked by linker.
 XX
 PS Claim 39; Page 46-47; 55pp; English.

XX
 CC sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of
 CC binding to two sites of its target protein. The protein comprises a first
 CC binding domain capable of binding to an inducing site on the target
 CC protein, a second binding domain capable of forming neutralising complex
 CC with an induced epitope of the target protein and a linker connecting the
 CC binding domains. sCD4-SCFv(17b) comprises a soluble CD4 fragment
 CC (containing domains D1 and D2) fused to a single chain Fv portion of
 CC antibody 17b via a linker. sCD4-SCFv(17b), its variant, analogue or
 CC mimetic is used for inactivating gp120 protein of HIV, and for
 CC neutralising HIV. It is also used for blocking and preventing the binding
 CC of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte
 CC CD4 and for inhibiting HIV replication. The chimeric proteins is
 CC therefore useful for treating HIV infection and also AIDS. It is are
 CC particularly useful in the prevention of infection during or immediately
 CC after HIV exposure (e.g., mother/infant transmission, post-exposure
 CC prophylaxis, and as a topical inhibitor) and for providing long term
 CC resistance to HIV infections and AIDS. Gene therapy is used to secrete
 CC the bispecific protein at mucosal surfaces, such as the vaginal, rectal
 CC or oral mucosa. The fusion proteins is highly potent, broadly cross-
 CC reactive with neutralising antibody with high in vivo activity and no PC-
 CC mediated undesirable targeting properties. When the fusion protein is
 CC substantially derived from human proteins, it has minimal immunogenicity
 CC and toxicity in humans which is of great value in prevention of infection
 CC during or immediately after HIV exposure
 XX
 SQ Sequence 507 AA;

Query Match 77.7%; Score 1023; DB 3; Length 507;
 Best Local Similarity 99.5%; Pred. No. 5,4e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVYLGGKGDVELTCTASOKKSIOFHMKNSNOIK 60
 DB 1 MNRGVPFRHLVLVQLALPAATQGNKVYLGGKGDVELTCTASOKKSIOFHMKNSNOIK 60
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKULKIEDSDTYICEVEDQKEEYOL 120
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKULKIEDSDTYICEVEDQKEEYOL 120
 QY 121 LVFGLTANSDTHLLOGQSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSDTHLLOGQSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWICTVLOQOKKVEFKIDIV 200
 DB 181 TWICTVLOQOKKVEFKIDIV 200

RESULT 71

AAR20152
 ID AAR20152 standard; protein; 519 AA.

XX AAR20152;

XX 25-MAR-2003 (revised)
 DT 31-MAR-1992 (first entry)
 XX

DE Human CD4 sequence encoded by PATY.6.

XX Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;
 KW acquired immune deficiency syndrome; AIDS related complex;
 KM T helper lymphocytes.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25
 PT /label= signal_sequence
 XX
 PN MO9118618-A.

PD 12-DEC-1991.

XX 25-MAY-1990; 90US-00529186.

PR 25-MAY-1990; 90US-00529186.

PA (BIOJ) BIOGEN INC.

PI Fisher RA, Hession C, Burkly LC;

DR WPI; 1992-007200/01.

DR N-PSDB; AAQ20327.

PT New immuno-therapeutic human CD4 variants and derivs. - elicit AB
 PT production to HIV gp.120, useful in treating, preventing and diagnosing
 PT AIDS, ARC and HIV infections.
 XX

PS Disclosure; Fig 28; 179pp; English.

XX The sequence was deduced from the DNA sequence of subclone PATY.6, contg.
 CC DNA coding for the full-length human CD4. The clone was constructed from
 CC plasmid pBG178A and pBG378 (both in US8802940). The DNA can be used to
 CC express recombinant CD4 and analogues for use in diagnosis and treatment
 CC of diseases caused by infective agents whose primary targets are T4+
 CC lymphocytes. See also AAR20148-R20155 and AAR21078. (Updated on 25-MAR-
 CC 2003 to correct PA field.)
 XX

SQ Sequence 519 AA;

Query Match 77.7%; Score 1023; DB 2; Length 519;
 Best Local Similarity 99.5%; Pred. No. 5,5e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVYLGGKGDVELTCTASOKKSIOFHMKNSNOIK 60
 DB 62 MNRGVPFRHLVLVQLALPAATQGNKVYLGGKGDVELTCTASOKKSIOFHMKNSNOIK 121
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKULKIEDSDTYICEVEDQKEEYOL 120
 DB 122 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKULKIEDSDTYICEVEDQKEEYOL 181
 QY 121 LVFGLTANSDTHLLOGQSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 182 LVFGLTANSDTHLLOGQSILTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 241
 QY 181 TWICTVLOQOKKVEFKIDIV 200
 DB 242 TWICTVLOQOKKVEFKIDIV 261

RESULT 72

AA51082
 ID AA51082 standard; protein; 616 AA.

XX AA51082;

XX 23-MAR-2000 (first entry)
 DT
 XX

DE Human fusion protein CD4Bgammal.

XX Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;

KW anti-human immunodeficiency virus; CD4Bgammal.

XX Homo sapiens.

OS Synthetic.

XX US6004781-A.

XX

PD 21-DEC-1999.
XX
PF 04-FEB-1994; 94US-00191708.
XX
PR 22-JAN-1988; 88US-00147351.
PR 23-JAN-1989; 89US-00295956.
PR 09-JUN-1992; 92US-0086781.
PR 12-APR-1993; 93US-00057952.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI: 2000-085792/07.
DR N-PSDB; AAZ44065.
XX
PT Fusion protein useful for the treatment of human immunodeficiency virus.
PS Example 1; Col 59-70; 39pp; English.
XX
CC This invention describes a novel nucleic acid (I) encoding a fusion
CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC chain (III). The products of the invention have anti-human
CC immunodeficiency virus (HIV) activity and are capable of binding to
CC gp120. The fusion protein is useful for treating human immunodeficiency
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC represents the fusion protein CD4Bgamma1 which is constructed from CD4
CC linked to human IgG1 upstream of the hinge region
XX
SQ Sequence 616 AA;

Query Match 77.7%; Score 1023; DB 3; Length 616;
Best Local Similarity 99.5%; Pred. No. 6.7e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVLOQOKKVEFKIDIV 200
DB 181 TWTCVLOQOKKVEFKIDIV 200

RESULT 73
AAV59172
ID AAV59172 standard; protein; 616 AA.
XX
AC AAV59172;
XX
DT 14-MAR-2000 (first entry)
XX
DE CD4-Ig fusion protein CD4Bgamma1.
XX
KM HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KM secreted protein; SIV infection; medicament.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CA1340741-C.
XX
PD 14-SEP-1999.
XX

PF 20-JAN-1989; 89CA-00588749.
XX
PR 20-JAN-1989; 89CA-00588749.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI: 2000-063015/06.
DR N-PSDB; AAZ48205.
XX
PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
PT the treatment of HIV or simian immunodeficiency virus infections.
XX
PS Example 1; Page 61-68; 89pp; English.
XX
CC The invention provides a fusion gene encoding a fusion protein that
CC comprises an extracellular CD4 DNA sequence or its fragment which binds
CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC the variable region has been replaced with the DNA sequence which encodes
CC extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC capable of being secreted. The fusion proteins are useful for treating
CC HIV or SIV infections in animals, preferably humans. They are also useful
CC for producing medicaments which can be used for treating HIV or SIV
CC infections in humans. The present sequence represents the fusion protein
CC CD4Bgamma1 where the CD4 is linked to human IgG1 at the BamI site
CC downstream from the hinge region
XX
SQ Sequence 616 AA;

Query Match 77.7%; Score 1023; DB 3; Length 616;
Best Local Similarity 99.5%; Pred. No. 6.7e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLESPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVLOQOKKVEFKIDIV 200
DB 181 TWTCVLOQOKKVEFKIDIV 200

RESULT 74
AAP93009
ID AAP93009 standard; protein; 631 AA.
XX
AC AAP93009;
XX
DT 25-MAR-2003 (revised)
DT 02-NOV-1992 (first entry)
XX
DE Genetic construct which encodes CD4 linked to human IgG1 at the Esp site
DE upstream of the hinge region (fusion protein CD4B-gamma-1).
XX
KM Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
KM diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
OS Homo sapiens.
XX
PN EP325262-A.
XX
PD 26-JUL-1989.
XX

PF 20-JAN-1989; 89EP-00100913.
 XX
 PR 22-JAN-1988; 88US-00147351.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B;
 XX
 DR WPI: 1989-214472/30.
 DR N-PSDB; AAN90357.
 XX
 PT Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
 PT infections or detecting HIV or SIV in sample.
 PS
 PS Example: Table 2, Page 24-33; 68pp; English.
 XX
 CC The fusion protein genes of the invention pref. comprise cDNA sequences
 CC which encode CD4 or a fragment which binds gp120 ligated to an expression
 CC plasmid which encodes an antibody in which the variable region of the
 CC gene has been deleted (see WO87-02671). The CD4 portion of the fusion
 CC protein may comprise the complete CD4 sequence, the 370 AA extracellular
 CC region and the membrane spanning domain, or the extracellular region. The
 CC Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
 CC specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Fmu, CD4E-
 CC gamma1, and CD4Mmu (No. 67608), pCD4P-gamma (No. 67609) and pCD4E-gamma-1
 CC (No. 67610). The plasmid containing (pCD4E-gamma-1) has been deposited in
 CC E. coli (MC1061/P3) at the ATCC under accession number 67610. (Updated on
 CC 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 631 AA;
 Query Match 77.7%; Score 1023; DB 1; Length 631;
 Best Local Similarity 99.5%; Pred. No. 6,9e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNRGVFPRHLLVQLALPAATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
 DB 1 MNRGVFPRHLLVQLALPAATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVLQNKQKVEFKIDIV 200
 RESULT 75
 AAB19508
 ID AAB19508 standard; protein; 631 AA.
 XX
 AC AAB19508;
 XX
 DT 09-JAN-2001 (first entry)
 XX
 DE CD4-IgG1 fusion protein CH4Bgammal.
 XX
 KM CD4; IgG1; human; CD4Bgammal; fusion protein; immunoglobulin; HIV; SIV;
 KM gp120; therapy; diagnosis.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Protein 1..395
 FT /note="CD4 extracellular region"
 FT Protein 400..631
 FT /note="IgG1 heavy chain"
 XX

PN US6117656-A.
 XX
 PD 12-SEP-2000.
 XX
 XX 07-JUN-1995; 95US-00479353.
 PF
 XX 22-JAN-1988; 88US-00147351.
 PR 23-JAN-1989; 89US-00299596.
 PR 09-JUN-1992; 92US-00896781.
 PR 12-APR-1993; 93US-00057952.
 PR 04-FEB-1994; 94US-00191708.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Seed B;
 XX
 DR WPI: 2000-586558/55.
 DR N-PSDB; AAB50661.
 XX
 PT CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
 PT SIV.
 PS
 PS Example 1; Col 29-42; 39pp; English.
 XX
 CC The present sequence is that of fusion protein CD4Bgammal comprising the
 CC extracellular portion of CD4, which binds to HIV gp120, linked at its C-
 CC terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
 CC encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge
 CC region (see AAB50661). Fusion protein CD4Bgammal and a nucleic acid
 CC encoding it are claimed. Also claimed are a vector comprising the nucleic
 CC acid, and a method of producing the fusion protein in secreted form using
 CC a transformed host cell. The fusion protein may further comprise a
 CC therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
 CC can be administered to an animal (including humans) for treatment of HIV
 CC or SIV infection, and can also be used in assays for HIV or SIV, imaging
 CC and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both
 CC complement-mediated and cell-mediated immunity
 XX
 SQ Sequence 631 AA;
 Query Match 77.7%; Score 1023; DB 3; Length 631;
 Best Local Similarity 99.5%; Pred. No. 6,9e-63;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNRGVFPRHLLVQLALPAATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
 DB 1 MNRGVFPRHLLVQLALPAATQGNKVVIGKGDVLTCTASQKKSIOFHMKNSNQIK 60
 QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
 DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
 QY 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 DB 121 LVFGLTANSPTHLLOGQSITLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
 QY 181 TWTCTVLQNKQKVEFKIDIV 200
 DB 181 TWTCTVLQNKQKVEFKIDIV 200
 RESULT 76
 AAY51079
 ID AAY51079 standard; protein; 631 AA.
 XX
 AC AAY51079;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DE Human fusion protein CD4Bgammal.
 XX
 KM Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
 KM anti-human immunodeficiency virus; CD4Bgammal.
 XX

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XX Homo sapiens.
OS Synthetic.
XX US604781-A.
XX 21-DEC-1999.
XX 04-FEB-1994; 94US-00191708.
XX 22-JAN-1988; 88US-00147351.
XX 23-JAN-1989; 89US-00299596.
XX 09-JUN-1992; 92US-00896781.
XX 12-APR-1993; 93US-00057952.
XX (GCHO ) GEN HOSPITAL CORP.
XX Seed B;
XX WPI: 2000-085792/07.
XX N-PSDB; AAZ44062.
XX Fusion protein useful for the treatment of human immunodeficiency virus.
XX Example 1; Col 29-42; 39pp; English.
XX This invention describes a novel nucleic acid (I) encoding a fusion
XX protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
XX and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
XX chain (III). The products of the invention have anti-human
XX immunodeficiency virus (HIV) activity and are capable of binding to
XX gp120. The fusion protein is useful for treating human immunodeficiency
XX virus (HIV) or simian immunodeficiency virus (SIV). This sequence
XX represents the fusion protein CD4Bgamma1 which is constructed from CD4
XX linked to human IgG1 upstream of the hinge region
XX
SQ Sequence 631 AA;
Query Match 77.7%; Score 1023; DB 3; Length 631;
Best Local Similarity 99.5%; Pred. No. 6.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLWDQGNFPIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLWDQGNFPIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPTHLLOQGSLLTLTSPGSSPSVQCSPRGKNIOGKTLTSSOLELQDSG 180
DB 121 LVFGLTANSDPTHLLOQGSLLTLTSPGSSPSVQCSPRGKNIOGKTLTSSOLELQDSG 180
QY 181 TWTCVTLONOKKVEFKIDIV 200
DB 181 TWTCVTLONOKKVEFKIDIV 200

RESULT 77
AAV59169
ID AAV59169 standard; protein; 631 AA.
XX
XX AAV59169;
XX
XX 14-MAR-2000 (first entry)
XX
XX CD4-Ig fusion protein CD4Bgamma1.
XX
XX HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
XX secreted protein; SIV infection; medicament.
XX
XX Synthetic.

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OS Homo sapiens.
XX CA1340741-C.
XX 14-SEP-1999.
XX 20-JAN-1989; 89CA-00588749.
XX 20-JAN-1989; 89CA-00588749.
XX (GCHO ) GEN HOSPITAL CORP.
XX Seed B;
XX WPI: 2000-063015/06.
XX N-PSDB; AAZ48202.
XX New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
XX the treatment of HIV or simian immunodeficiency virus infections.
XX Example 1; Page 37-46; 89pp; English.
XX The invention provides a fusion gene encoding a fusion protein that
XX comprises an extracellular CD4 DNA sequence or its fragment which binds
XX to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
XX sequence of an Ig heavy or light chain, where the DNA sequence encoding
XX the variable region has been replaced with the DNA sequence which encodes
XX extracellular CD4 or its gp120 binding fragment. The fusion protein is
XX capable of being secreted. The fusion proteins are useful for treating
XX HIV or SIV infections in animals, preferably humans. They are also useful
XX for producing medicaments which can be used for treating HIV or SIV
XX infections in humans. The present sequence represents the fusion protein
XX CD4Bgamma1 where the CD4 is linked to human IgG1 at the Esp site upstream
XX of the hinge region
XX
SQ Sequence 631 AA;
Query Match 77.7%; Score 1023; DB 3; Length 631;
Best Local Similarity 99.5%; Pred. No. 6.9e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLWDQGNFPIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLWDQGNFPIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPTHLLOQGSLLTLTSPGSSPSVQCSPRGKNIOGKTLTSSOLELQDSG 180
DB 121 LVFGLTANSDPTHLLOQGSLLTLTSPGSSPSVQCSPRGKNIOGKTLTSSOLELQDSG 180
QY 181 TWTCVTLONOKKVEFKIDIV 200
DB 181 TWTCVTLONOKKVEFKIDIV 200

RESULT 78
AAP93008
ID AAP93008 standard; protein; 729 AA.
XX
XX AAP93008;
XX
XX 25-MAR-2003 (revised)
XX
XX 02-NOV-1992 (first entry)
XX
XX Genetic construct which encodes CD4 linked to human IgG1 at the Hind3
XX site upstream of the CH1 region (fusion protein CD4H-gamma-1).
XX
XX Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
XX diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX

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OS Homo sapiens.
XX EP325262-A.
XX
XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-00100913.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 1989-214472/30.
XX N-PSDB; AAN90356.
XX
XX Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
XX infections or detecting HIV or SIV in sample.
XX
XX Example; Table 1, Page 12-23; 68pp; English.
XX
XX The fusion protein genes of the invention pref. comprise cDNA sequences
XX which encode CD4 or a fragment which binds gp120 ligated to an expression
XX plasmid which encodes an antibody in which the variable region of the
XX gene has been deleted (see WO87-02671). The CD4 portion of the fusion
XX protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX region and the membrane spanning domain, or the extracellular region. The
XX Ig heavy chain is pref. from IgM, IgG1 or IgG3. The following are
XX specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Pmu, CD4E-
XX gamma1, and CD4Mmu (No. 67608), pCD4P-gamma (No. 67609) and pCD4E-gamma-1
XX (No. 67610). The plasmid containing (pCD4H-gamma-1) has been deposited in
XX E. coli (MC1061/P3) at the ATCC under accession number 67611. (Updated on
XX 25-MAR-2003 to correct PA field.)
XX
XX Sequence 729 AA;
XX
XX Query Match 77.7%; Score 1023; DB 1; Length 729;
XX Best Local Similarity 99.5%; Pred. No. 8.1e-63;
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILGNQGSFLTKGSPSKINDRADSRSLMDGNPFLIINKLKIEDSDTYICEVEDQKEEVOL 120
XX 61 ILGNQGSFLTKGSPSKINDRADSRSLMDGNPFLIINKLKIEDSDTYICEVEDQKEEVOL 120
XX
XX 121 LVFGLTANSDTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLLEIDSG 180
XX 121 LVFGLTANSDTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLLEIDSG 180
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX Db
XX
XX RESULT 79
XX AAB19507
XX ID AAB19507 standard; protein; 729 AA.
XX
XX AAB19507;
XX
XX 09-JAN-2001 (first entry)
XX
XX CD4-IgG1 fusion protein CH4Hgamma1.
XX
XX CD4; IgG1; human; CD4Hgamma1; fusion protein; immunoglobulin; HIV; SIV;
XX gp120; therapy; diagnosis.
XX
XX Homo sapiens.
XX

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FH Key Location/Qualifiers
FT Protein 1..395
FT /note= "CD4 extracellular region"
FT Protein 400..729
FT /note= "IgG1 heavy chain"
XX
XX US6117656-A.
XX
XX 12-SEP-2000.
XX
XX 07-JUN-1995; 95US-00479353.
XX
XX 22-JAN-1988; 88US-00147351.
XX 23-JAN-1989; 89US-00295956.
XX 09-JUN-1989; 89US-00896781.
XX 12-APR-1993; 93US-00057952.
XX 04-FEB-1994; 94US-00191708.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 2000-586558/55.
XX N-PSDB; AAA50660.
XX
XX CD4-Immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
XX SIV.
XX
XX Example 1; Col 13-30; 39pp; English.
XX
XX The present sequence is that of fusion protein CD4Hgamma1 comprising the
XX extracellular portion of CD4, which binds to HIV gp120, linked at its C-
XX terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
XX encoding CD4 was linked to IgG1 DNA at the Hind III site upstream of the CH1
XX region (see AAA50660). Fusion protein CD4Hgamma1 and a nucleic acid
XX encoding it are claimed. Also claimed are a vector comprising the nucleic
XX acid, and a method of producing the fusion protein in secreted form using
XX a transformed host cell. The fusion protein may further comprise a
XX therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
XX can be administered to an animal (including humans) for treatment of HIV
XX or SIV infection, and can also be used in assays for HIV or SIV, imaging
XX and tissue stains. IgG1 fusion proteins such as CD4Hgamma1 provide both
XX complement-mediated and cell-mediated immunity
XX
XX Sequence 729 AA;
XX
XX Query Match 77.7%; Score 1023; DB 3; Length 729;
XX Best Local Similarity 99.5%; Pred. No. 8.1e-63;
XX Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNSNQIK 60
XX
XX 61 ILGNQGSFLTKGSPSKINDRADSRSLMDGNPFLIINKLKIEDSDTYICEVEDQKEEVOL 120
XX 61 ILGNQGSFLTKGSPSKINDRADSRSLMDGNPFLIINKLKIEDSDTYICEVEDQKEEVOL 120
XX
XX 121 LVFGLTANSDTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLLEIDSG 180
XX 121 LVFGLTANSDTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLSSVQLLEIDSG 180
XX
XX 181 TWICTVLOKQKVEFKIDIV 200
XX 181 TWICTVLOKQKVEFKIDIV 200
XX
XX Db
XX
XX RESULT 80
XX AAY51078
XX ID AAY51078 standard; protein; 729 AA.
XX
XX AAY51078;
XX

```

```

DT 23-MAR-2000 (first entry)
XX
DE Human fusion protein CD4H-1.
XX
KW Fusion protein; human; CD4; IgG1; immunoglobulin; gp120;
KM anti-human immunodeficiency virus; CD4H-1.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6004781-A.
XX
PD 21-DEC-1999.
XX
PF 04-FEB-1994; 94US-00191708.
XX
PR 22-JAN-1988; 88US-00147351.
PR 23-JAN-1989; 89US-00299596.
PR 09-JUN-1992; 92US-00896781.
PR 12-APR-1993; 93US-00057952.
XX
PA (GENO ) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-085792/07.
DR N-PSDB; AAZ44061.
XX
PT Fusion protein useful for the treatment of human immunodeficiency virus.
XX
PS Example 1; Col 15-30; 39pp; English.
XX
CC This invention describes a novel nucleic acid (I) encoding a fusion
CC protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II)
CC and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light
CC chain (III). The products of the invention have anti-human
CC immunodeficiency virus (HIV) activity and are capable of binding to
CC gp120. The fusion protein is useful for treating human immunodeficiency
CC virus (HIV) or simian immunodeficiency virus (SIV). This sequence
CC represents the fusion protein CD4H-1 which is constructed from CD4 linked
CC to human IgG1 upstream of the CH1 region
XX
SQ Sequence 729 AA;

Query Match 77.7%; Score 1023; DB 3; Length 729;
Best Local Similarity 99.5%; Pred. No. 8.1e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRHLLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPPRHLLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPVQCRSPRGKNIQGGKTLSSVQLDLDSG 180
DB 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPVQCRSPRGKNIQGGKTLSSVQLDLDSG 180
QY 181 TWICTVLONOKKVEFKIDIV 200
DB 181 TWICTVLONOKKVEFKIDIV 200

```

RESULT 81
AA59168
ID AA59168 standard; protein; 729 AA.

XX
AC AA59168;
DT 14-MAR-2000 (first entry)
XX

```

DE CD4-Ig fusion protein CD4Hgamma1.
XX
KW HIV; extracellular; CD4; gp120; immunoglobulin; Ig; fusion protein;
KM secreted protein; SIV infection; medicament.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN CA1340741-C.
XX
PD 14-SEP-1999.
XX
PF 20-JAN-1989; 89CA-00588749.
XX
PR 20-JAN-1989; 89CA-00588749.
XX
PA (GENO ) GEN HOSPITAL CORP.
XX
PI Seed B;
XX
DR WPI; 2000-063015/06.
DR N-PSDB; AAZ48201.
XX
PT New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in
XX the treatment of HIV or simian immunodeficiency virus infections.
XX
PS Example 1; Page 25-36; 89pp; English.
XX
CC The invention provides a fusion gene encoding a fusion protein that
CC comprises an extracellular CD4 DNA sequence or its fragment which binds
CC to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA
CC sequence of an Ig heavy or light chain, where the DNA sequence encoding
CC the variable region has been replaced with the DNA sequence which encodes
CC extracellular CD4 or its gp120 binding fragment. The fusion protein is
CC capable of being secreted. The fusion proteins are useful for treating
CC HIV or SIV infections in animals, preferably humans. They are also useful
CC for producing medicaments which can be used for treating HIV or SIV
CC infections in humans. The present sequence represents the fusion protein
CC CD4Hgamma1 where the CD4 is linked to human IgG1 at the Hind3 site
CC upstream of the CH1 region
XX
SQ Sequence 729 AA;

Query Match 77.7%; Score 1023; DB 3; Length 729;
Best Local Similarity 99.5%; Pred. No. 8.1e-63;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPPRHLLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
DB 1 MNRGVPPRHLLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPVQCRSPRGKNIQGGKTLSSVQLDLDSG 180
DB 121 LVFGLTANSDTHLLQGOQLTLTLESPPGSSPVQCRSPRGKNIQGGKTLSSVQLDLDSG 180
QY 181 TWICTVLONOKKVEFKIDIV 200
DB 181 TWICTVLONOKKVEFKIDIV 200

```

RESULT 82
AAR26530
ID AAR26530 standard; protein; 435 AA.

XX
AC AAR26530;
DT 25-MAR-2003 (revised)
DT 28-JAN-1993 (first entry)
XX

```
DE Sequence of one chain of a CD4-gamma 1 chimeric heavy chain homodimer.
XX
XX CD4-gamma 1 chimeric heavy chain homodimer; expression vector; HIV;
KM therapy; diagnostic agent; inhibition.
XX
OS Synthetic.
XX
FH Key
FH Region 1.204
FT /label=CD4
FT /note="1..25 = prerregion"
FT 205..219
FT /label=hinge
FT Region 220..329
FT /label=CH2
FT Region 330..436
FT /label=CH3
XX
XX WC9213559-A1.
XX
XX 20-AUG-1992.
XX
XX 10-FEB-1992; 92WO-US001152.
XX
XX 08-FEB-1991; 91US-00654205.
XX
XX (PROG-) PROGENICS PHARM INC.
XX
XX Beaudry GA, Maddon PJ;
XX
XX WPI; 1992-299758/36.
XX
XX N-PSDB; AAQ27830.
XX
XX CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector -
PT for preventing and creating HIV infection useful as a diagnostic agent.
XX
XX Example; Fig 3; 89pp; English.
XX
XX Human CD4 cDNA was excised from pSPET4 and cloned into M13mp18. The 2 kb
CC PetI/PstI fragment from pBR lambda.1 contg. the human lambda.1 heavy
CC chain gene (contg. the hinge, CH2 and CH3 exons) was isolated and cloned
CC into the BAP-treated M13mp18/CD4 vector. To obtain a CD4-lambda.1
CC chimeric heavy chain gene, oligonucleotide-mediated site-directed
CC mutagenesis was performed to juxtapose the CD4 and lambda.1 heavy chain
CC DNA sequences, ligating the CD4 sequence in frame to the hinge exon. The
CC DNA was then cloned into pCDNA-1 to produce CD4-IgG1-pCDNA1 (ATCC 40951).
CC (Updated on 25-MAR-2003 to correct FN field.)
XX
XX Sequence 435 AA;
SQ
Query Match 77.6%; Score 1021.5; DB 2; Length 435;
Best Local Similarity 86.8%; Pred. No. 5.8e-63;
Matches 204; Conservative 1; Mismatches 21; Indels 9; Gaps 1;
QY 2 NRGVPRHLILVQLALLPATQGNKVVLGKGDVVELTCTASQKKSIOFHMKNNOIKI 61
DB 1 NRGVPRHLILVQLALLPATQGNKVVLGKGDVVELTCTASQKKSIOFHMKNNOIKI 60
QY 62 LSGNSFLTKGPKSLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 121
DB 61 LSGNSFLTKGPKSLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 122 VFGLTANSDTHLLQGOSLTLTLESPPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSGT 181
DB 121 VFGLTANSDTHLLQGOSLTLTLESPPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSGT 180
QY 182 WTCTVLQNKQKVEFKIDIV-----PRASALPAPPTGSALPDPQTASALPDP 227
DB 181 WTCTVLQNKQKVEFKIDIVLAFEPKSCDKTHCPCEPAPPELLGGSVFLFPKP 235
RESULT 83
ADE65841
```

```
ID ADE65841 standard; protein; 458 AA.
XX
XX ADE65841;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX Human CD4 receptor.
DE
XX
XX Human; CD4 receptor; receptor; protein-protein interaction;
KM protein array; PDZ domain; drug target screening.
XX
OS Homo sapiens.
XX
XX US2003170723-A1.
XX
XX 11-SEP-2003.
XX
XX 06-MAR-2002; 2002US-00092138.
XX
XX 06-MAR-2002; 2002US-00092138.
XX
XX (SATO/) SATO T.
XX
XX Sato T;
XX
XX WPI; 2003-852032/79.
XX
XX
XX Preparing a protein array useful for screening drug targets comprises
PT depositing an array of a first protein on substrate, and applying a
PT second protein comprising an amino acid sequence that binds to a domain
PT of the first protein.
XX
XX Disclosure; SEQ ID NO 25; 60pp; English.
XX
XX The invention relates to a method for preparing a protein array based on
CC protein-protein interaction, by depositing an array of a first protein
CC comprising a PDZ domain on a substrate, and applying a second protein
CC comprising an amino acid sequence that binds to the PDZ domain of the
CC first protein. The method is useful for preparing protein arrays based on
CC biochemical protein-protein interactions. Arrays produced by this method
CC are useful for screening drug targets. This sequence represents the human
CC CD4 receptor, used in the method of the invention.
XX
XX Sequence 458 AA;
SQ
Query Match 77.5%; Score 1021; DB 7; Length 458;
Best Local Similarity 99.0%; Pred. No. 6.7e-63;
Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NRGVPRHLILVQLALLPATQGNKVVLGKGDVVELTCTASQKKSIOFHMKNNOIK 60
DB 1 NRGVPRHLILVQLALLPATQGNKVVLGKGDVVELTCTASQKKSIOFHMKNNOIK 60
QY 61 IISGNSFLTKGPKSLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 IISGNSFLTKGPKSLNDRADSRSLMDQGNPFLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVOCRSRPGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
RESULT 84
AAP93012
ID AAP93012 standard; protein; 614 AA.
XX
XX AAP93012;
AC
XX
XX 25-MAR-2003 (revised)
DT
```



```
DT 03-AUG-1992 (first entry)
XX Genetic construct which encodes CD4 linked to human IgG1 at the BstI site
DE downstream from the hinge region (fusion protein CD4lambda1).
DE
XX Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
XX diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
XX Homo sapiens.
XX
XX EPJ25262-A.
XX
XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-00100913.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 1989-214472/30.
XX
XX N-PSDB; AAN90360.
XX
XX Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
XX infections or detecting HIV or SIV in sample.
XX
XX Example; Table 5, Page 48-55; 68pp; English.
XX
XX The fusion protein genes of the invention pref. comprises cDNA sequences
XX which encode CD4 or a fragment which binds gp120 ligated to an expression
XX plasmid which encodes an antibody in which the variable region of the
XX gene has been deleted (see W087-02671). The CD4 portion of the fusion
XX protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX region and the membrane spanning domain, or the extracellular region. The
XX Ig heavy chain is pref. from IGM, IgG1 or IgG3. The following are
XX specifically claimed: fusion proteins CD4lambda1, CD4muu, CD4pmu,
XX CD4Elambda1, and CD4muu (No. 67608), pCD4lambda1 (No. 67609) and
XX pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 614 AA;
SQ
Query Match 77.3%; Score 1018; DB 1; Length 614;
Best Local Similarity 99.0%; Pred. No.1.5e-62;
Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRHLLLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
RESULT 85
AAP93011
ID AAP93011 standard; protein; 481 AA.
XX
XX AAP93011;
XX
XX AC AAP93011;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-AUG-1992 (first entry)
XX
```

```
DE Genetic construct which encodes CD4 linked to human IGM at the PstI site
DE upstream of the CH2 region (fusion protein CD4Pmu).
DE
XX Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
XX diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX
XX Homo sapiens.
XX
XX EPJ25262-A.
XX
XX 26-JUL-1989.
XX
XX 20-JAN-1989; 89EP-00100913.
XX
XX 22-JAN-1988; 88US-00147351.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Seed B;
XX
XX WPI; 1989-214472/30.
XX
XX N-PSDB; AAN90359.
XX
XX Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
XX infections or detecting HIV or SIV in sample.
XX
XX Example; Table 4, Page 41-47; 68pp; English.
XX
XX The fusion protein genes of the invention pref. comprises cDNA sequences
XX which encode CD4 or a fragment which binds gp120 ligated to an expression
XX plasmid which encodes an antibody in which the variable region of the
XX gene has been deleted (see W087-02671). The CD4 portion of the fusion
XX protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX region and the membrane spanning domain, or the extracellular region. The
XX Ig heavy chain is pref. from IGM, IgG1 or IgG3. The following are
XX specifically claimed: fusion proteins CD4lambda1, CD4muu, CD4pmu,
XX CD4Elambda1, and CD4muu (No. 67608), pCD4lambda1 (No. 67609) and
XX pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 481 AA;
SQ
Query Match 77.1%; Score 1015; DB 1; Length 481;
Best Local Similarity 99.0%; Pred. No.1.8e-62;
Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNRGVPRHLLLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPRHLLLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSGLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
RESULT 86
AAB07768
ID AAB07768 standard; protein; 394 AA.
XX
XX AAB07768;
XX
XX AC AAB07768;
XX
XX DT 07-NOV-2000 (first entry)
XX
XX DE The soluble extracellular domain of the T4 glycoprotein.
XX
XX Human; T4 glycoprotein; human immunodeficiency virus; HIV;
```

```

KM envelope glycoprotein; AIDS; virus binding.
XX
OS Homo sapiens.
XX
PN US6093539-A.
XX
PD 25-JUL-2000.
XX
PF 06-JUN-1995; 95US-00466368.
XX
PR 21-AUG-1986; 86US-00898587.
PR 11-JUN-1991; 91US-00713564.
PR 06-JUL-1992; 92US-00909021.
PR 12-DEC-1994; 94US-00354452.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Madden PJ, Chess L, Axel R, Weiss R, McDougal JS, Littman DR;
XX
XX WPI; 2000-505203/45.
DR N-PSDB; AAA59351.
XX
XX New isolated nucleic acid encoding a human T cell surface protein and the
PT soluble surface T4 glycoprotein that it encodes, useful as prophylaxis
PT for treating a subject infected with human acquired immune deficiency
PT syndrome virus.
XX
XX
PS Disclosure; Col 11-14; 69pp; English.
XX
XX The present sequence represents an aqueous-soluble polypeptide comprising
CC a portion of a human T4 glycoprotein. The portion specifically forms a
CC complex with a human immunodeficiency virus (HIV) envelope glycoprotein.
CC The DNA is useful for producing the soluble surface T4 glycoprotein. The
CC soluble surface T4 glycoprotein is useful as a therapeutic agent, i.e. as
CC prophylaxis for treating a subject infected with an HIV virus. Thus, the
CC soluble T4 glycoprotein is useful for treating human AIDS. The soluble T4
CC glycoprotein is also useful in diagnostic or screening assays, e.g. for
CC screening inhibitors of virus binding, or for detecting and quantitating
CC T4, T4+ cells and antibodies to T4, which are of diagnostic value for
CC AIDS.
XX
XX Sequence 394 AA;
SQ
Query Match 76.8%; Score 1012; DB 3; Length 394;
Best Local Similarity 98.5%; Pred. No. 2,4e-62;
Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNQIK 60
DB 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNQIK 60
QY 61 ILNGQSSFLTKGSPSKINDRADSRSLMDQGNPPLIINKIKIEDSDTYICEVEDQKEVOL 120
DB 61 ILNGQSSFLTKGSPSKINDRADSRSLMDQGNPPLIINKIKIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180
QY 181 TWICTVLQNKQKVEFKIDIV 200
DB 181 TWICTVLQNKQKVEFKIDIV 200
RESULT 87
AAR06373 standard; protein; 458 AA.
XX
AC AAR06373;
XX
DT 31-OCT-2002 (revised)
DT 20-DEC-1990 (first entry)
XX

```

```

DE T4 encoded by plasmid p170-2.
XX
XX plasmid p170-2; soluble T4 protein; AIDS; ARC; HIV.
XX
OS Synthetic.
XX
FH Key
FH Peptide 1..23
FT /label= hydrophobic/secretory signal
FT 24..117
FT /label= extracellular
FT /note= "homology to V-regions"
FT 118..132
FT /label= extracellular
FT /note= "homology to J-regions"
FT 133..397
FT /label= extracellular
FT /note= "glycosylated region"
FT 398..418
FT /label= transmembrane sequence
FT /note= "hydrophobic"
FT 419..458
FT /label= intracytoplasmic
FT /note= "very hydrophilic"
XX
XX WO9008198-A.
XX
XX 26-JUL-1990.
XX
XX 18-JAN-1989; 89US-00300096.
XX
XX 18-JAN-1989; 89US-00300096.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Letvin NA;
XX
XX WPI; 1990-254040/33.
DR N-PSDB; AAQ05607.
XX
XX Treating or preventing AIDS, ARC or HIV infection - by administering an
PT immunologically effective amt. of soluble T4 protein.
XX
PS Disclosure; Fig 1, 121pp; English.
XX
XX Soluble T4 can be produced by truncating the CDS to remove the
CC transmembrane and cytoplasmic domains. The soluble forms may be modified
CC to increase their immunogenicity by addition of an adjuvant such as
CC incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction
CC and elicits anti-soluble T4 antibody production. Soluble T4 proteins
CC include the following polypeptide fragments: amino acids 1-385, 24-385,
CC Met-24-385, 24-397, 1-400 and Met-24-400. See also AAQ05608. (Updated on
CC 31-OCT-2002 to add missing OS field.)
XX
XX Sequence 458 AA;
SQ
Query Match 76.6%; Score 1009; DB 2; Length 458;
Best Local Similarity 99.0%; Pred. No. 4,5e-62;
Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNQIK 60
DB 1 MNRGVFRRHLVLVQLALPAATQGNKVVLGKKGDTVELTCTASQKKSIOFHMKNQIK 60
QY 61 ILNGQSSFLTKGSPSKINDRADSRSLMDQGNPPLIINKIKIEDSDTYICEVEDQKEVOL 120
DB 61 ILNGQSSFLTKGSPSKINDRADSRSLMDQGNPPLIINKIKIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLOQSLTLTLSPGSSPSVQCRSPRKNIQGGKTLVSQLELDQSG 180
QY 181 TWICTVLQNKQKVEFKIDIV 200

```

Db 181 TWTCVTVLQNGKVKVEFKIDIV 200

RESULT 88

AAP94703
ID AAP94703 standard; protein; 524 AA.

XX AAP94703;

XX 25-MAR-2003 (revised)

DT 22-MAR-1991 (first entry)

XX Sequence encoded by T4 lymphocyte cDNA obtained from PBL clone lambda-203

DE -4.

XX HIV; soluble T4; immunotherapeutic; prophylactic; diagnostic; AIDS; ARC.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 67 /note= "AA DESIGNATED NUMBER -23"

FT Misc-difference 90 /note= "AA DESIGNATED NUMBER 1"

FT Misc-difference 92 /note= "MATURE N-TERMINUS"

XX MO8901940-A.

XX PD 09-MAR-1989.

XX PF 01-SEP-1988; 88WO-US002940.

XX 04-SEP-1987; 87US-00094322.

XX 07-JAN-1988; 88US-00141649.

XX (BIOJ) BIOGEN INC.

XX PI Fisher RA, Gilbert W, Sato VL, Flavell RA, Maraganore JM;

XX DR WPI; 1989-085519/11.

XX N-PSDB; AAN90642.

XX DNA sequences coding for soluble T4-like polypeptide(s) - used in

XX immunotherapeutic and immunosuppressive comps. and for preventing,

XX creating or detecting AIDS.

XX PS Disclosure; Fig 3; 207pp; English.

XX The polypeptides encoded are useful in immunotherapeutic, prophylactic

XX and diagnostic comps. They can be used to purify HIV from a sample. The

XX soluble T4 protein-based comps. are useful in treating immunodeficient

XX patients suffering from diseases caused by agents whose primary targets

XX are T4+ lymphocytes. They can be used for preventing, treating or

XX detecting AIDS, ARC and HIV infection. (Updated on 25-MAR-2003 to correct

XX PR field.)

XX SQ Sequence 524 AA;

Query Match 76.6%; Score 1009; DB 1; Length 524;

Best Local Similarity 99.0%; Pred. No. 5.3e-62;

Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAATQGNKVVLGKGDVVELTCTASQKSIQFHMKNNOIK 60

Db 67 MNRGVPRHLLLVQLALPAAATQGNKVVLGKGDVVELTCTASQKSIQFHMKNNOIK 126

QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVQL 120

Db 127 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVQL 186

QY 121 LVFGLTANSPTHLILQGSGLTLTLESPPSSPVQCRSPRGNKIGGKTLTSLVSQLDQSG 180

Db 187 LVFGLTANSPTHLILQGSGLTLTLESPPSSPVQCRSPRGNKIGGKTLTSLVSQLDQSG 246

RESULT 89

AAR07640
ID AAR07640 standard; protein; 2458 AA.

XX AAR07640;

XX 31-OCT-2002 (revised)

DT 20-DEC-1990 (first entry)

XX Deduced protein sequence of p170-2 comprising T4.

DE plasmid p170-2; soluble T4 protein; AIDS; ARC; HIV.

XX Synthetic.

XX Key Location/Qualifiers

FT Protein 400..858 /label= T4 surface glycoprotein

XX MO9008198-A.

XX PD 26-JUL-1990.

XX PF 18-JAN-1989; 89US-00300096.

XX 18-JAN-1989; 89US-00300096.

XX (HARD) HARVARD COLLEGE.

XX PI Letvin NA;

XX DR WPI; 1990-254040/33.

XX N-PSDB; AAQ05607.

XX Treating or preventing AIDS, ARC or HIV infection - by administering an

XX immunologically effective amt. of soluble T4 protein.

XX Disclosure; Fig 1; 121pp; English.

XX Entire sequence from T4-encoding plasmid p170-2. It is almost identical

XX to the sequence published by Maddon et al (1985) with the exception of

XX three codon changes. At T4 amino acid residue 3, (posn.403 of entire

XX sequence) Lys is encoded in stead of Asn. At posn. 64, (posn.464) Arg

XX replaces Trp and at posn. 231, (posn. 631) Ser replaces Phe. Soluble T4

XX can be produced by truncating the CDS to remove the transmembrane and

XX cytoplasmic domains. The soluble forms may be modified to increase their

XX immunogenicity by addition of an adjuvant such as incomplete Freund's

XX adjuvant. The T4 interferes with HIV/T4 interaction and elicits anti-

XX soluble T4 antibody production. See also AAQ05608. (Updated on 31-OCT-

XX 2002 to add missing OS field.)

XX SQ Sequence 2458 AA;

Query Match 76.6%; Score 1009; DB 2; Length 2458;

Best Local Similarity 99.0%; Pred. No. 2.9e-61;

Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLLVQLALPAAATQGNKVVLGKGDVVELTCTASQKSIQFHMKNNOIK 60

Db 400 MNRGVPRHLLLVQLALPAAATQGNKVVLGKGDVVELTCTASQKSIQFHMKNNOIK 459

QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVQL 120

Db 460 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIETSDTYICEVEDQKEEVQL 519

QY 121 LVFGLTANS DTHLLQGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 180
 DB 520 LVFGLTANS DTHLLQGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 579
 QY 181 TWCTVLOQNKVKVEFKIDIV 200
 DB 580 TWCTVLOQNKVKVEFKIDIV 599

RESULT 90

AAR04031
 ID AAR04031 standard; protein; 2458 AA.

AC AAR04031;
 XX 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 29-MAY-1990 (first entry)

XX Full length T4 encoded by plasmid p170-2.

XX Soluble T4; p170-2; anti-retroviral agent; AIDS; ARC; HIV; AZT.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 423

FT /note= "Trp of Madden et al replaced by Arg"

FT Misc-difference 425

FT /note= "Asp of Madden et al replaced by Lys"

FT Misc-difference 653

FT /note= "Phe of Madden et al replaced by Ser"

PN MO8911860-A.

PD 14-DEC-1989.

PF 08-JUN-1989; 89WO-US002453.

XX 10-JUN-1988; 88US-00204645.

PR 20-APR-1989; 89US-00341080.

XX (BIOU) BIOGEN NV INC.

PA (GEHO) GEN HOSPITAL CORP.

PA (BIOU) BIOGEN INC.

PA (BIOU) BIOGEN INC.

XX Fisher RA, Schooley RT, Hirsch MS, Johnson VA, Walker BD;

PI WPI; 1990-007302/01.

XX N-PSDB; AA003005.

DR Combinations of soluble T4 protein and anti-retroviral agent - having

XX synergistic activity in treatment and prevention of AIDS, arc and HIV

PT infection.

XX Disclosure; Fig 1; 100pp; English.

PS The sequence differs from that determined by PJ Madden et al., [Cell, 42

XX CC pp. 93-104 (1985)] in three places due to three nucleotide substitutions.

CC The Asp reported at position 3 by Madden et al. was the result of a

CC sequencing error [DR Litzman et al. Cell, 55, p.541 (1988)]. X = stop

CC codon. The sequence was deduced from the cDNA insert of p170-2. Soluble

CC T4 constructs may be produced by truncating this sequence to give

CC fragments from position 400 to 799, removing the transmembrane and

CC intracytoplasmic domains whilst retaining the extracellular region

CC responsible for HIV binding. The sol. T4 is combined with an anti-viral

CC agent such as AZT. See also AA003006. (Updated on 31-OCT-2002 to add

CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 2458 AA;

SO Query Match 76.6%; Score 1009; DB 2; Length 2458;

Best Local Similarity 99.0%; Pred. No. 2,9e-61;
 Matches 198; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKRGVPRHLILVLTALIPATQGNKVYLGKGGPTVELTCASOKKSIQFMKNSNOIK 60
 DB 400 MKRGVPRHLILVLTALIPATQGNKVYLGKGGPTVELTCASOKKSIQFMKNSNOIK 459
 QY 61 ILNGGSPFLTKGPKSLNBRADSRSLMDQGNPFLIIKNLIKEDSPYICEVEDEKEEYVL 120
 DB 460 ILNGGSPFLTKGPKSLNBRADSRSLMDQGNPFLIIKNLIKEDSPYICEVEDEKEEYVL 519
 QY 121 LVFGLTANS DTHLLQGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 180
 DB 520 LVFGLTANS DTHLLQGSLTLTLSPGSSPVQCRSPRGKNIQGGKTLTSSVQLLEIDSG 579
 QY 181 TWCTVLOQNKVKVEFKIDIV 200
 DB 580 TWCTVLOQNKVKVEFKIDIV 599

RESULT 91

AAR04910
 ID AAR04910 standard; protein; 458 AA.

XX AAR04910;

XX 31-OCT-2002 (revised)

DT 02-OCT-1990 (first entry)

XX T4 protein as encoded by p170.2.

DE T4 protein; immunotoxin; Pseudomona endotoxin A; AIDS; HIV; ARC;

XX angiotensin; fusion protein.

XX Synthetic.

OS Key Location/Qualifiers

FT Peptide 1..26

FT /label= signal peptide

FT Protein 27..458

FT /label= T4 protein

FT Misc-difference replace(87,N)

FT /note= "differs from Madden et al"

FT Misc-difference replace(254,F)

FT /note= "differs from Madden et al"

XX MO9004414-A.

XX 03-MAY-1990.

PD 18-OCT-1988; 88US-00259355.

XX 18-OCT-1988; 88US-00259355.

XX (BIOU) BIOGEN INC.

PA Meade HM, Lobb RR, Gates LL, Winkler G;

PA WPI; 1990-163876/21.

XX N-PSDB; AA004555.

DR New immunotoxin contg. soluble T4 protein components and toxin - esp.

XX Pseudomonas endotoxin A, for treating or controlling AIDS and related

XX conditions, and new DNA sequences.

XX Disclosure; Page 7; -pp; English.

PS The T4 protein encoded by p170.2 is almost identical to that reported by

XX P.J. Madden et al [Cell, 42, pp 93-104 (1985)]. The Madden sequence was

XX revised in 1988 to correct a DNA sequencing error at AA 3 (corrected from

XX Asp to Lys; see M12807 in GenBank). The DNA may be truncated (to remove

XX transmembrane and intracellular regions) and/or modified by SDM, pref. so

XX the prod. extends from AAs 3-183 of the mature protein. This DNA can then

CC be ligated to a toxin DNA esp. angiogenin, or a fragment of Pseudomonas
CC exotoxin A conig. the translocation and ADP-ribosylation domains. The
CC hybrid DNA can then be inserted into an expression vector and used to
CC produce recombinant fusion protein which is useful for preventing or
CC treating AIDS, ARC, and HIV infections. The T4 protein is an HIV receptor
CC which binds to virus or to infected cells carrying the gp120/160 marker
CC antigen, so provides v. specific targeting with minimal damage to non-
CC target cells. (updated on 31-OCT-2002 to add missing OS field.)

XX Sequence 458 AA;

Query Match 76.2%; Score 1004; DB 2; Length 458;

Best Local Similarity 98.5%; Pred. No. 1e-61; Mismatches 0; Gaps 0;

Matches 197; Conservative 1; Indels 2; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQONQKVEFKIDIV 200
DB 181 TWCTCTVLQONQKVEFKIDIV 200

RESULT 92

AAR11285 AAR11285 standard; protein; 458 AA.

XX AAR11285;

XX 25-MAR-2003 (revised)
XX 09-JAN-2003 (revised)
XX 29-APR-1991 (first entry)

DE gp120 binding protein.

XX Human; CD4; AIDS; HIV1; SIV; gp120.

XX Unidentified.

XX Key Location/Qualifiers

FT MISC-difference 59 /label= Thr or Ile
FT MISC-difference 93 /label= Thr or Pro

PN EP414178-A.

XX 27-FEB-1991.

XX 18-AUG-1990; 90EP-00115877.

XX 23-AUG-1989; 89US-00397782.

XX (GEHO) GEN HOSPITAL CORP.

XX Seed B, Camerini D;

XX WPI; 1991-059419/09.

XX N-PSDB; AAQ10887.

XX New non-human primate and human CD4 or gp120 molecules - used to treat
XX HIV or SIV and immunoglobulin and gp120 binding molecules from new fusion
XX proteins.

PS Claim 17; Page 57; 87pp; English.

XX The fragment from residues 1-134 is also independently claimed. The sub-
XX fragment (and the complete polypeptide) can bind to HIV gp120. See also
XX AAQ10885-6, AAQ10888. (Updated on 09-JAN-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 458 AA;

Query Match 76.1%; Score 1002; DB 2; Length 458;

Best Local Similarity 98.0%; Pred. No. 1.4e-61; Mismatches 4; Indels 0; Gaps 0;

Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVLGKGGDTVELTCTASQKKSIOFHKNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWCTCTVLQONQKVEFKIDIV 200
DB 181 TWCTCTVLQONQKVEFKIDIV 200

RESULT 93

AAR20151 AAR20151 standard; protein; 399 AA.

XX AAR20151;

XX 25-MAR-2003 (revised)
XX 31-MAR-1992 (first entry)

DE Chimpanzee sol. CD4 encoded by pSQ200.

XX Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;
XX acquired immune deficiency syndrome; AIDS related complex;
XX T helper lymphocytes.

XX Pan troglodytes.

XX Key Location/Qualifiers

FT Peptide 1..25 /label= signal_sequence
FT WO9118618-A.

PN 12-DEC-1991.

XX 25-MAY-1990; 90US-00529186.

XX 25-MAY-1990; 90US-00529186.

XX (BIOG) BIOGEN INC.

XX Fisher RA, Hession C, Burkly LC;

XX WPI; 1992-007200/01.

XX N-PSDB; AAQ20326.

XX New immuno-therapeutic human CD4 variants and derivs. - elicit AB
XX production to HIV gp.120, useful in treating, preventing and diagnosing
XX AIDS, ARC and HIV infections.
XX Claim 15; Fig 21; 179pp; English.

XX The sequence was deduced from the DNA sequence of clone pSQ200 which was

CC obcd. by cloning using a reverse transcriptase/PCR amplification
CC procedure with a non-specific oligo dt to prime first strand synthesis.
CC The PCR fragments were ligated into sequencing plasmid pNN08 (see
CC AAQ020326). The DNA sequence can be used to express recombinant soluble CD4
CC and analogues for use in diagnosis and treatment of diseases caused by
CC infective agents whose primary targets are T4 lymphocytes. See also
CC AAR20148-R20155 and AAR21078. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX

SQ Sequence 399 AA;

Query Match 75.9%; Score 999; DB 2; Length 399;
Best Local Similarity 97.5%; Pred. No. 1,9e-61;

Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQTK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQTK 60
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSPTHLLOGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCTVLOQNKVEFKIDIV 200
DB 181 TWTCTVLOQNKVEFKIDIV 200

RESULT 94

AAR10988
ID AAR10988 standard; protein; 458 AA.

XX AC AAR10988;
XX DT 25-MAR-2003 (revised)
XX DT 29-APR-1991 (first entry)
XX DE Chimpanzee CD4 protein.
XX KM Chimpanzee; CD4; AIDS; HIV1; SIV.
XX OS Pan troglodytes.
XX FH Key
XX FT Protein
XX FT Location/Qualifiers
XX FT 26
XX FT /label= mature CD4
XX PN EP414178-A.
XX PD 27-FEB-1991.
XX PF 18-AUG-1990; 90EP-00115877.
XX PR 23-AUG-1989; 89US-00397782.
XX PA (GENO) GEN HOSPITAL CORP.
XX PI Seed B, Camerini D;
XX PI WPI; 1991-059419/09.
XX DR N-PSDB; AAQ10886.

XX New non-human primate and human CD4 or gp120 molecules - used to treat
XX HIV or SIV and immunoglobulin and gp120 binding molecules from new fusion
XX proteins.
XX PS Claim 4; Page 45; 87pp; English.

CC The CD4 protein or HIV gp120-binding fragments of it are used to detect

CC and treat HIV and SIV infection. Animals which can be treated include
CC humans, baboons, orang-utans, chimpanzees, gorillas and rhesus monkeys.
CC The chimpanzee CD4 is 99 per cent homologous to its human counterpart,
CC possessing 5 amino acid substitutions in the 433 residue predicted mature
CC polypeptide. See also AAQ10885, AAQ10887-8. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX

SQ Sequence 458 AA;

Query Match 75.9%; Score 999; DB 2; Length 458;
Best Local Similarity 97.5%; Pred. No. 2.3e-61;

Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQTK 60
DB 1 MNRGVPFRHLVLVQLALPAATQGNKVVLGKKGDTVELCTASQKKSIOFHKNSNQTK 60
QY 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTCKPSKLNDRADSRSLMDQGNFPLIIKNLIKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSPTHLLOGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCTVLOQNKVEFKIDIV 200
DB 181 TWTCTVLOQNKVEFKIDIV 200

RESULT 95

AAR20150
ID AAR20150 standard; protein; 400 AA.

XX AC AAR20150;
XX DT 25-MAR-2003 (revised)
XX DT 31-MAR-1992 (first entry)
XX DE Chimpanzee sol. CD4 sequence from pSQ205.
XX KM Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;
XX KM acquired immune deficiency syndrome; AIDS related complex;
XX OS Pan troglodytes.
XX FH Key
XX FT Peptide
XX FT Location/Qualifiers
XX FT 1..25
XX FT /label= signal_sequence
XX PN MO9118618-A.
XX PD 12-DEC-1991.
XX PF 25-MAY-1990; 90US-00529186.
XX PR 25-MAY-1990; 90US-00529186.
XX PA (BIOJ) BIOGEN INC.
XX PI Fisher RA, Hession C, Burkly LC;
XX PI WPI; 1992-007200/01.
XX DR N-PSDB; AAQ20325.

XX New immuno-therapeutic human CD4 variants and derivs. - elicit AB
XX production to HIV gp.120, useful in treating, preventing and diagnosing
XX AIDS, ARC and HIV infections.
XX PS Claim 15; Fig 20; 179pp; English.

CC The sequence was deduced from the DNA sequence of clone pSQ205 which was

obed. by cloning using a reverse transcriptase/PCR amplification procedure. The DNA sequence can be used to express recombinant soluble CC CD4 and analogues for use in diagnosis and treatment of diseases caused CC by infective agents whose primary targets are T4+ lymphocytes. See also CC AAB20148-R20155 and AAB21078. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 400 AA;

Query Match 75.5%; Score 994; DB 2; Length 400;
Best Local Similarity 97.0%; Pred. No. 4,36-61;
Matches 194; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASQKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASQKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTGGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
DB 61 ILGNQGSFLTGGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLQGGSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLQGGSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVVLQNKQKVEFKIDIV 200
DB 181 TWTCVVLQNKQKVEFKIDIV 200

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RESULT 96

AAB93010
ID AAB93010 standard; protein: 399 AA.

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XX AC AAB93010;
XX DT 25-MAR-2003 (revised)
XX DT 03-AUG-1992 (first entry)
XX DE Genetic construct which encodes CD4 linked to human IGM at the Met2 site
XX DE upstream of the CH1 region (fusion protein CD4Mmu).
XX KM Fusion protein; immunoglobulin-like molecule; HIV; SIV; therapy;
XX KM diagnosis; CD4; gp120; binding fragment; glycoprotein; variable region.
XX OS Homo sapiens.
XX PN EP325262-A.
XX PD 26-JUL-1989.
XX PF 20-JAN-1989; 89EP-00100913.
XX PR 22-JAN-1988; 88US-00147351.
XX (GEHO ) GEN HOSPITAL CORP.
XX PA Seed B;
XX PI WPI; 1989-214472/30.
XX DR N-PSDB; AAN90358.
XX FT Immunoglobulin-CD4 fusion proteins - used for treating HIV or SIV
XX FT infections or detecting HIV or SIV in sample.
XX PS Example; Table 3, Page 34-40; 68pp; English.
XX CC The fusion protein genes of the invention pref. comprises cDNA sequences
XX CC which encode CD4 or a fragment which binds gp120 ligated to an expression
XX CC plasmid which encodes an antibody in which the variable region of the
XX CC gene has been deleted (see W087-02671). The CD4 portion of the fusion
XX CC protein may comprise the complete CD4 sequence, the 370 AA extracellular
XX CC region and the membrane spanning domain, or the extracellular region.

```

CC Ig heavy chain is pref. from IGM, IgG1 or IgG3. The following are CC specifically claimed: fusion proteins CD4lambda1, CD4Mmu, CD4PMu, CC CD4lambda1, and CD4Mmu (No. 67608), PCDA1lambda (No. 67609) and CC PCDA1lambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 399 AA;

Query Match 74.6%; Score 982; DB 1; Length 399;
Best Local Similarity 97.0%; Pred. No. 2,96-60;
Matches 194; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASQKSIQFHKNSNQIK 60
DB 1 MNRGVPRHLLVQLALPPAATQGNKVVLGKKGDVVELTCTASQKSIQFHKNSNQIK 60
QY 61 ILGNQGSFLTGGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
DB 61 ILGNQGSFLTGGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLQGGSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLQGGSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCVVLQNKQKVEFKIDIV 200
DB 181 TWTCVVLQNKQKVEFKIDIV 200

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RESULT 97

AAB19511
ID AAB19511 standard; protein: 616 AA.

```

XX AC AAB19511;
XX DT 09-JAN-2001 (first entry)
XX DE CD4-IgG1 fusion protein CH4Bgamma1.
XX KM CD4; IgG1; human; CD4Bgamma1; fusion protein; immunoglobulin; HIV; SIV;
XX KM gp120; therapy; diagnosis.
XX OS Homo sapiens.
XX PN US6117656-A.
XX PD 12-SEP-2000.
XX PF 07-JUN-1995; 95US-00479353.
XX PR 22-JAN-1988; 88US-00147351.
XX PR 23-JAN-1989; 89US-00299596.
XX PR 09-JUN-1992; 92US-00896781.
XX PR 12-APR-1993; 93US-00057952.
XX PR 04-FEB-1994; 94US-00191708.
XX (GEHO ) GEN HOSPITAL CORP.
XX PA Seed B;
XX PI WPI; 2000-586558/55.
XX DR N-PSDB; AAA50664.
XX CC CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
XX CC SIV.
XX PS Example 1; Col 59-70; 39pp; English.

```

CC The present sequence is that of fusion protein CD4Bgam1 comprising the
CC extracellular portion of CD4, which binds to HIV gp120, linked at its C-
CC terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA
CC encoding CD4 was linked to IgG1 DNA at the BamI site downstream of the
CC hinge region (see A4A5066). Fusion protein CD4Bgam1 and a nucleic acid
CC encoding it are claimed. Also claimed are a vector comprising the nucleic
CC acid, and a method of producing the fusion protein in secreted form using
CC a transformed host cell. The fusion protein may further comprise a
CC therapeutic agent, radiolabel or NMR imaging agent. The fusion protein
CC can be administered to an animal (including humans) for treatment of HIV
CC or SIV infection, and can also be used in assays for HIV or SIV, imaging
CC and tissue stains. IgG1 fusion proteins such as CD4Bgam1 provide both
CC complement-mediated and cell-mediated immunity
CC
XX

SQ Sequence 616 AA;

Query Match 73.6%; Score 969; DB 3; Length 616;
Best Local Similarity 96.5%; Pred. No. 3.8e-59;
Matches 193; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPAATQGNKVLGKGGDTVELCTASOKKSIOFHKNKSNQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVLGKGGDTVELCTASOKKSIOFHKNKSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLIKIDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLIKIDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWICTVLOQNKVEFKIDIV 200
DB 181 TWICTVLOQNKVEFKIDIV 200

RESULT 98

AAR20154
ID AAR20154 standard; protein; 400 AA.

XX AAR20154;

DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 31-MAR-1992 (first entry)

DE SOL. rhesus-human chimeric CD4 encoded by pDG100.

XX Human immunodeficiency virus; HIV; gp 120; AIDS; ARC; glycoprotein;
KM acquired immune deficiency syndrome; AIDS related complex; monkey;
XX T helper lymphocytes.

XX Macaca mulatta; (Rhesus).

OS Homo sapiens.

OS Chimeric.

Location/Qualifiers

FT Region 1..131
FT /note="rhesus CD4 encoded by pS0146 (AAQ20328)"
FT Peptide 1..25
FT /label= signal_sequence
FT Region 132..400
FT /note="human CD4 encoded by pB3191 (US8802940)"

XX MO9118618-A.
XX
XX 12-DEC-1991.
XX
XX 25-MAY-1990; 90US-00529186.
XX
XX 25-MAY-1990; 90US-00529186.
XX
XX

PA (BIOI) BIOGEN INC.
XX
XX Fisher RA, Hession C, Burkly LC;
PI
XX
XX WPI, 1992-007200/01.
DR
XX N-PSDB; AAQ20329.
DR

PT New immuno-therapeutic human CD4 variants and derivs. - elicit AB
PT production to HIV gp.120, useful in treating, preventing and diagnosing
PT AIDS, ARC and HIV infections.

XX Claim 14; Fig 13; 179pp; English.

XX The sequence is encoded by pDG100, chimeric plasmid prepd. from human and
CC rhesus derived CD4 DNA. The plasmid can be used to express recombinant
CC sol. chimeric CD4 for use in diagnosis and treatment of diseases caused
CC by infective agents whose primary targets are T4+ lymphocytes. See also
CC AAR20148-R2015 and AAR21078. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 24-OCT-2003 to standardise OS field)
XX

SQ Sequence 400 AA;

Query Match 72.4%; Score 954; DB 2; Length 400;
Best Local Similarity 92.0%; Pred. No. 2.6e-58;
Matches 184; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALPAATQGNKVLGKGGDTVELCTASOKKSIOFHKNKSNQIK 60
DB 1 MNRGVPRHLLVQLALPAATQGNKVLGKGGDTVELCTASOKKSIOFHKNKSNQIK 60
QY 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLIKIDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGSPSKLNDRADSRSLMDQGNPFLIIKNLIKIDSDTYICEVEDQKEEYQL 120
QY 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLTGQSLTTLTSPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWICTVLOQNKVEFKIDIV 200
DB 181 TWICTVLOQNKVEFKIDIV 200

RESULT 99

AAR15149
ID AAR15149 standard; protein; 458 AA.

XX AAR15149;

DT 25-MAR-2003 (revised)
DT 24-FEB-1992 (first entry)

DE CD4 coordinate system.

XX Gelsolin; fusion protein; diagnosis; AIDS.

XX Homo sapiens.

XX Key Location/Qualifiers
FT Domain 1..25
FT /label= hydrophobic/secretory_signal
FT Domain 26..132
FT /label= first Ig-related_domain
FT /note="extracellular"

FT Disulfide-bond 41..109
FT Domain 133..202
FT /label= second Ig-related_domain
FT /note="extracellular"

FT Disulfide-bond 155..184
FT Domain 203..318
FT /label= third Ig-related_domain
FT /note="extracellular"

FT Domain 319..395


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FT /label= fourth Ig-related_domain
FT /note= "extracellular"
FT Disulfide-bond 328..370
FT Domain 396..416
FT /label= hydrophobic/transmembrane_sequence
FT 417..458
FT /label= very_hydrophilic/intracytoplasmic
XX
XX MO9117170-A.
XX
XX PD 14-NOV-1991.
XX
XX PF 04-MAY-1990; 90US-00520368.
XX
XX PR 04-MAY-1990; 90US-00520368.
XX
XX PA (BIOJ ) BIOGEN INC.
XX
XX PI Peglnsky RB, Rosa MD, Stoszel TP;
XX
XX DR WPI; 1991-353711/48.
XX
XX DR N-PSDB; AAQ14931.
XX
XX PT New multi-meric and hetero-multi-meric geleolin fusion constructs - used
XX to treat and diagnose AIDS, ARC and HIV infection.
XX
XX PS Disclosure; Fig 3A-3D; 131pp; English.
XX
XX CC The CD4 polypeptides useful in the constructs include all CD4
XX polypeptides which bind to or otherwise inhibit gp120 and gp160. These
XX CC include fragments lacking the transmembrane domain. In particular it is
XX CC Cda 1-111; 1-Cyell1; 1-Cyell80; 1-181; 1-183; 1-187; 1-345 or 1-375 (from
XX CC mature protein). See also AAQ14931-35 and AA15151. (Updated on 25-MAR-
XX CC 2003 to correct PA field.)
XX
XX SQ Sequence 458 AA;

Query March 71.8%; Score 946; DB 2; Length 458;
Best Local Similarity 92.0%; Pred. No. 1,1e-57;
Matches 184; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MNRGVFPHLLVQLALLPATOGNKVVLGKSGDTVELTCTASQKSIQFHMKNQIK 60
DB 1 MNRGVFPHLLVQLALLPATOGNKVVLGKSGDTVELTCTASQKSIQFHMKNQIK 60
QY 61 ILGNQGSFLLTKGPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLLTKGPKLNDRADSRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDPHLLQGSULTITLSPSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSDPHLLQGSULTITLSPSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 121 LVFGLTANSDPHLLQGSULTITLSPSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSDPHLLQGSULTITLSPSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCTVLQNKVFEKIDIV 200
DB 181 TWTCTVLQNKVFEKIDIV 200
QY 181 TWTCTVLQNKVFEKIDIV 200
DB 181 TWTCTVLQNKVFEKIDIV 200

RESULT 100
AAP90833
ID AAP90833 standard; protein; 384 AA.
XX
XX AAP90833;
XX
XX AC 25-MAR-2003 (revised)
XX
XX DT 01-AUG-1990 (first entry)
XX
XX DE Amino acid sequence of a soluble T4-like (sr4) polypeptide encoded by a
XX portion of clone p199-7 (PL mutec.rsr4).
XX
XX KW HIV; immunotherapeutic; prophylactic; soluble T4-like polypeptide;
XX diagnostic; p199-7 (PL mutec.rsr4).
```

```
OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Misc-difference 10
FT /note= "Initiating Met"
XX
XX MO8901940-A.
XX
XX PD 09-MAR-1989.
XX
XX PF 01-SEP-1988; 88WO-US002940.
XX
XX PR 04-SEP-1987; 87US-00094322.
XX
XX PR 07-JAN-1988; 88US-00141649.
XX
XX PA (BIOJ ) BIOGEN INC.
XX
XX PI Fisher RA, Gilbert W, Sato VL, Flavell RA, Maraganore JM;
XX
XX DR WPI; 1989-085519/11.
XX
XX DR N-PSDB; AAN90643.
XX
XX PT DNA sequences coding for soluble T4-like polypeptide(s) - used in
XX PT immuno:therapeutic and immunosuppressive comps. and for preventing,
XX PT treating or detecting AIDS.
XX
XX PS Disclosure; Page 7; 207pp; English.
XX
XX CC It is the protein sequence encoded by the rsr4 sequence. It is claimed in
XX CC the patent. It is useful in immunotherapeutic, prophylactic and
XX CC diagnostic comps. It can be used to purify HIV from a sample. (Updated
XX CC on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 384 AA;

Query March 69.6%; Score 916; DB 1; Length 384;
Best Local Similarity 100.0%; Pred. No. 1,1e-55;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QGNKRVVLGKGGDTVELTCTASQKSIQFHMKNQIKILGNQGSFLLTKGPKLNDRADSR 83
DB 11 QGNKRVVLGKGGDTVELTCTASQKSIQFHMKNQIKILGNQGSFLLTKGPKLNDRADSR 70
QY 84 RSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOLVGLTRANSPTHLLQGSULTTL 143
DB 71 RSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOLVGLTRANSPTHLLQGSULTTL 130
QY 144 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLQNKVFEKIDIV 200
DB 131 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCTVLQNKVFEKIDIV 187

Search completed: August 3, 2004, 13:08:20
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 13:14:00 ; Search time 21.8374 Seconds
(without alignments)
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Title: SEQ6
Perfect score: 1317
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Searched: 1291235 seqs, 313682936 residues
Total number of hits satisfying chosen parameters: 1291235

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 125 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1038	78.8	310	8	US-08-485-163-7
2	1038	78.8	310	8	US-09-766-995-6
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4	1032.5	78.4	432	8	US-08-485-163-2
5	1030.5	78.2	530	8	US-08-485-163-5
6	1030.5	78.2	530	9	US-09-766-995-4
7	1029	78.1	203	10	US-09-939-537-31
8	1029	78.1	398	10	US-09-939-537-29
9	1029	78.1	402	14	US-10-097-044A-1
10	1029	78.1	457	11	US-09-891-119A-9
11	1029	78.1	462	10	US-09-939-537-5
12	1029	78.1	462	11	US-09-243-008-5
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17	1023	77.7	458	12	US-10-151-274-3	Sequence 3, Appli
18	1023	77.7	458	14	US-10-103-597A-39	Sequence 39, Appli
19	1023	77.7	458	14	US-10-188-444-39	Sequence 39, Appli
20	1023	77.7	458	8	US-10-207-655-170	Sequence 170, App
21	1021	77.5	458	14	US-08-681-219-27	Sequence 27, Appli
22	1021	77.5	458	11	US-09-230-111C-25	Sequence 25, Appli
23	1021	77.5	458	14	US-09-922-138-25	Sequence 25, Appli
24	1012	76.8	397	11	US-09-891-119A-2	Sequence 2, Appli
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26	916	69.6	434	14	US-10-097-044A-4	Sequence 4, Appli
27	903	68.3	178	14	US-10-073-118-26	Sequence 26, Appli
28	899	68.3	178	9	US-09-934-060A-26	Sequence 26, Appli
29	899	68.3	370	9	US-09-759-841-6	Sequence 6, Appli
30	899	68.3	590	9	US-09-934-060A-13	Sequence 13, Appli
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34	494	37.5	94	11	US-09-891-119A-10	Sequence 10, Appli
35	486	36.9	93	14	US-10-105-545-26	Sequence 26, Appli
36	475	36.1	612	14	US-10-125-692-10	Sequence 10, Appli
37	337	25.6	84	9	US-09-135-238B-8	Sequence 8, Appli
38	332	25.2	240	9	US-09-997-165-2	Sequence 2, Appli
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47	133	10.1	535	15	US-10-108-60A-4247	Sequence 4247, Ap
48	131.5	10.0	1477	14	US-10-274-583-20	Sequence 20, Appli
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54	131.5	10.0	1498	12	US-10-243-552-899	Sequence 899, App
55	131	9.9	374	16	US-10-311-823-16	Sequence 16, Appli
56	131	9.9	442	16	US-10-311-823-12	Sequence 12, Appli
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94	125	9.5	332	9	US-09-993-687-517	Sequence 517, App
95	125	9.5	332	10	US-09-989-774-517	Sequence 517, App
96	125	9.5	332	10	US-09-978-189-216	Sequence 216, App
97	125	9.5	332	10	US-09-997-653-517	Sequence 517, App
98	125	9.5	332	10	US-09-993-667-517	Sequence 517, App
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106	125	9.5	332	10	US-09-978-608A-216	Sequence 216, App
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111	125	9.5	332	10	US-09-997-513-517	Sequence 517, App
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113	125	9.5	332	10	US-09-978-403A-216	Sequence 216, App
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117	125	9.5	332	10	US-09-997-559-517	Sequence 517, App
118	125	9.5	332	10	US-09-997-661-517	Sequence 517, App
119	125	9.5	332	10	US-09-999-833A-216	Sequence 216, App
120	125	9.5	332	10	US-09-981-915A-216	Sequence 216, App
121	125	9.5	332	10	US-09-990-443-517	Sequence 517, App
122	125	9.5	332	10	US-09-978-824-216	Sequence 216, App
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124	125	9.5	332	10	US-09-997-628-517	Sequence 517, App
125	125	9.5	332	10	US-09-997-663-517	Sequence 517, App

ALIGNMENTS

RESULT 1
 US-08-485-163-7
 : Sequence 7, Application US/08485163
 : Publication NO. US20020098191A1
 : GENERAL INFORMATION:
 : APPLICANT: Beaudry, Gary A.
 : APPLICANT: Maddon, Paul J.
 : TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Cooper & Dunham LLP
 : STREET: 1185 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10036
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.24
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/485,163
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 514
 : ATTORNEY/AGENT INFORMATION:
 : NAME: White, John P.
 : REGISTRATION NUMBER: 28,678
 : REFERENCE/DOCKET NUMBER: 37690-II-1-PCt-US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 278-0400

[illegible]

TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
JS-08-485-163-7

Query Match	78.8%;	Score 1038;	DB 8;	length 310;
Best Local Similarity	85.7%;	Pred. No. 1.3e-74;		
Matches 209; Conservative	4;	Mismatches 19;	Indels 12;	Gaps 1;

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Db	1	MNRVPRRLHLLVLTQLALLPAAATGKNVYLGGKSDTYELTCTAAOKKS	IOGHMKNNSNOIX	60
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Db	121	LVPELTANSDPHLLIQGSLTLTLESPGSSPSVOCSPRGKNIQGGKTLVSQLELODGS		180
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Qy	241	SFLI		244
Db	229	VCLL		232

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RESULT 2
US-09-766-995-6
; Sequence 6, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-1GG2 IMMUNOCONJ
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 2048/41215-CB/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/766,995
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 310
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-766-995-6

```

Query Match	78.8%	Score 1038	DB 9	Length 310
Best Local Similarity	85.7%	Pred. No. 1,38-74		
Matches	209	Conservative	4	Mismatches 19
			Indels	12
			Gaps	1

QY	1	MNRGVPFRHLHLVLQALLP	ATAGNRYVLGKKGDYELTCT	ASOKSIQFHMKNQNIK	60
DB	1	MNRGVPFRHLHLVLQALLP	ATAGKQKRYVLGKKGDYELTCT	ASOKSIQFHMKNQNIK	60
QY	61	ILGNQGSFLTYGPKSLNDR	ADSRSLNDQGNFLLIKNLK	IEDSDTYICEVEDQKEEYQL	120
DB	61	ILGNQGSFLTYGPKSLNDR	ADSRSLNDQGNFLLIKNLK	IEDSDTYICEVEDQKEEYQL	120
QY	121	LVFGLTNSDTHLLIQGOSL	TLTSSPCGSSPVQCRSPR	GNIGQKTLVSQLELODQSG	180
DB	121	LVFGLTNSDTHLLIQGOSL	TLTSSPCGSSPVQCRSPR	GNIGQKTLVSQLELODQSG	180

Oy	181	TWTCVLNOKKVEKIDIVPASALPAPTOSALPDPTASALDPDPPASALPALAVI	24
Db	181	TWTCVLNOKKVEKIDIVLALFVYAP-----SVFIPEDEQLKSGTASV	228
Oy	241	SFL 244	
Db	229	VCLL 232	
RESULT 3			
Oy	US-08-485-163-3	US-08-485-163-3	
Db	Sequence 3, Application US/08485163	Sequence 3, Application US/08485163	
Oy	Publication No. US20020098191A1	Publication No. US20020098191A1	
Db	GENERAL INFORMATION:	GENERAL INFORMATION:	
Oy	APPLICANT: Beauty, Gary A.	APPLICANT: Beauty, Gary A.	
Db	APPLICANT: Maddon, Paul J.	APPLICANT: Maddon, Paul J.	
Oy	TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS	TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS	
Db	NUMBER OF SEQUENCES: 10	NUMBER OF SEQUENCES: 10	
Oy	CORRESPONDENCE ADDRESS:	CORRESPONDENCE ADDRESS:	
Db	ADDRESSEE: Cooper & Dunham LLP	ADDRESSEE: Cooper & Dunham LLP	
Oy	STREET: 1185 Avenue of the Americas	STREET: 1185 Avenue of the Americas	
Db	CITY: New York	CITY: New York	
Oy	STATE: New York	STATE: New York	
Db	COUNTRY: USA	COUNTRY: USA	
Oy	ZIP: 10036	ZIP: 10036	
Db	COMPUTER READABLE FORM:	COMPUTER READABLE FORM:	
Oy	MEDIUM TYPE: Floppy disk	MEDIUM TYPE: Floppy disk	
Db	COMPUTER: IBM PC compatible	COMPUTER: IBM PC compatible	
Oy	OPERATING SYSTEM: PC-DOS/MS-DOS	OPERATING SYSTEM: PC-DOS/MS-DOS	
Db	SOFTWARE: Patent In Release #1.24	SOFTWARE: Patent In Release #1.24	
Oy	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	
Db	APPLICATION NUMBER: US/08/485,163	APPLICATION NUMBER: US/08/485,163	
Oy	FILING DATE: 07-JUN-1995	FILING DATE: 07-JUN-1995	
Db	CLASSIFICATION: 514	CLASSIFICATION: 514	
Oy	ATTORNEY/AGENT INFORMATION:	ATTORNEY/AGENT INFORMATION:	
Db	NAME: White, John P.	NAME: White, John P.	
Oy	REGISTRATION NUMBER: 28,678	REGISTRATION NUMBER: 28,678	
Db	REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US	REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US	
Oy	TELECOMMUNICATION INFORMATION:	TELECOMMUNICATION INFORMATION:	
Db	TELEPHONE: (212) 278-0400	TELEPHONE: (212) 278-0400	
Oy	TELEFAX: (212) 391-0525	TELEFAX: (212) 391-0525	
Db	TELEX:	TELEX:	
Oy	INFORMATION FOR SEQ ID NO: 3:	INFORMATION FOR SEQ ID NO: 3:	
Db	SEQUENCE CHARACTERISTICS:	SEQUENCE CHARACTERISTICS:	
Oy	LENGTH: 432 amino acids	LENGTH: 432 amino acids	
Db	TYPE: amino acid	TYPE: amino acid	
Oy	STRANDEDNESS: unknown	STRANDEDNESS: unknown	
Db	TOPOLOGY: unknown	TOPOLOGY: unknown	
Oy	MOLECULE TYPE: protein	MOLECULE TYPE: protein	
Db	ORIGINAL SOURCE:	ORIGINAL SOURCE:	
Oy	ORGANISM: homo sapien	ORGANISM: homo sapien	
Db	CELL TYPE: lymphocyte	CELL TYPE: lymphocyte	
Oy	US-08-485-163-3	US-08-485-163-3	
Db	Query Match	78.4% Score 1032.5; DB 8; Length 432;	
Oy	Best Local Similarity 88.0%; Pred. No. 5.6e-74;	Best Local Similarity 88.0%; Pred. No. 5.6e-74;	
Db	Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2	Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2	
Oy	1	MNRGVPFRHLILVLOLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHWKSNQIK	60
Db	1	MNRGVPFRHLILVLOLALLPAATQGNKVVLGKGGDTVELTCTASQKKSIOFHWKSNQIK	60
Oy	61	ILGNQGSPLTKPKSKINDPADRRSLMDGNEPLIIKNLKIDSDPIYCEVEDQKEEVL	120
Db	61	ILGNQGSPLTKPKSKINDPADRRSLMDGNEPLIIKNLKIDSDPIYCEVEDQKEEVL	120
Oy	121	LVFGILTANSDTHLQGSQSLTTLTLESPGSSPSVQCRSPKGNKIQGKTLISVQLLEQDSG	180
Db	121	LVFGILTANSDTHLQGSQSLTTLTLESPGSSPSVQCRSPKGNKIQGKTLISVQLLEQDSG	180
Oy	181	TWTCVLNOKKVEKIDIV---PPASALPAPTGSALPDPTASALDPDPPA	230
Db	181	TWTCVLNOKKVEKIDIV---PPASALPAPTGSALPDPTASALDPDPPA	230

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DB 181 TWCTCTVLQNGKKVEFKIDIVLAFERKCCVECP-----CPAPVA 221

RESULT 4
US-09-766-995-2
; Sequence 2, Application US/09766995
; Patent No. US20020052481A1
GENERAL INFORMATION:
APPLICANT: Graham P. Allway et al.
TITLE OF INVENTION: NON-PEPTIDYL NOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJ
FILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: homo saapians
US-09-766-995-2

Query Match 78.4%; Score 1032.5; DB 9; Length 432;
Best Local Similarity 88.0%; Pred. No. 5,66-74;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLILVQLALLPATQGNKRVLGKGDIVELTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLILVQLALLPATQGNKRVLGKGDIVELTCTASQKKSIOFHMKNNOIK 60
QY 61 ILNGQSFLLTGPSPKNDRAADRSRLMDQGNFLLITNLKTESDPTVCEVEDQKEEVOL 120
DB 61 ILNGQSFLLTGPSPKNDRAADRSRLMDQGNFLLITNLKTESDPTVCEVEDQKEEVOL 120
QY 121 LVFGITANSPTDHLIQGOSLTLTLESPPGSSPSVOCSPRGKNIQGGKTLISVSQLELODSG 180
DB 121 LVFGITANSPTDHLIQGOSLTLTLESPPGSSPSVOCSPRGKNIQGGKTLISVSQLELODSG 180
QY 181 TWCTCTVLQNGKKVEFKIDIV---PRASALPAPPTGSALPDPOTSALPDPPAA 230
DB 181 TWCTCTVLQNGKKVEFKIDIVLAFERKCCVECP-----CPAPVA 221

RESULT 5
US-08-485-163-5
; Sequence 5, Application US/08485163
; Publication No. US20020098191A1
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-485-163-5

Query Match 78.2%; Score 1030.5; DB 8; Length 530;
Best Local Similarity 84.8%; Pred. No. 1.1e-73;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60
DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIDSDTYICEVEDQKEEYQL 120
QY 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVOCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVOCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALALAVI 240
DB 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALALAVI 240
QY 241 SFLL 244
DB 230 GCLV 233

RESULT 6
US-09-766-995-4
Sequence 4, Application US/09766995
Patent No. US20020052481A1
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOLETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES
FILE REFERENCE: 2048/41215-CB/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 530
TYPE: PRT
ORGANISM: homo sapiens
US-09-766-995-4

Query Match 78.2%; Score 1030.5; DB 9; Length 530;
Best Local Similarity 84.8%; Pred. No. 1.1e-73;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60
DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIDSDTYICEVEDQKEEYQL 120
DB 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNLIKIDSDTYICEVEDQKEEYQL 120
QY 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVOCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVOCRSPRGKNIQGGKTLVSQLELDQSG 180

DB 121 LVFGILTANSDTHLQGSITLTLESPPGSSPVOCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALALAVI 240
DB 181 TWTCTVLQNKQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALALAVI 240
QY 241 SFLL 244
DB 230 GCLV 233

RESULT 7
US-09-939-537-31
Sequence 31, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
Kolanas, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Biling LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Biling, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-939-537-31

Query Match 78.1%; Score 1029; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60
DB 1 MNRGVPFRHLVLVQLALPPATQGNKVVLGKKGDVVELTCTASQKSIQFHMKNNOIK 60

Qy	6	ILNQSGFLTKGSKINDBADSRSLMDGNFLLIKULKIEDSPTYICEVEDKEEVL	120
Db	61	ILNQSGFLTKGSKINDRADSRSLMDGNFLLIKULKIEDSPTYICEVEDKEEVL	120
Qy	121	LVEGLTANSDTHLLOQOSLTLTLESPPGSSPSVOCRSPRGKNIQGGKTLVSQLELDDSG	180
Db	121	LVEGLTANSDTHLLOQOSLTLTLESPPGSSPSVOCRSPRGKNIQGGKTLVSQLELDDSG	180
Qy	181	TWTCVTLQONOKVEFKIDIV	200
Db	181	TWTCVTLQONOKVEFKIDIV	200

RESULT 8

1 Sequence 29, Application US/09939537
 2 Publication No. US20030138410A1
 3 GENERAL INFORMATION:
 4 APPLICANT: Seed, Brian
 5 Banapur, Babak
 6 Romeo, Charles
 7 Kolanus, Waldemar
 8 TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
 9 CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
 10
 11 NUMBER OF SEQUENCES: 53
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Clark & Elbing LLP
 14 STREET: 176 Federal Street
 15 CITY: Boston
 16 STATE: MA
 17 COUNTRY: USA
 18 ZIP: 02110
 19
 20 COMPUTER READABLE FORM:
 21 MEDIUM TYPE: Diskette
 22 COMPUTER: IBM Compatible
 23 OPERATING SYSTEM: DOS
 24 SOFTWARE: FastSeq for Windows Version 2.0
 25
 26 CURRENT APPLICATION DATA:
 27 APPLICATION NUMBER: US/09/939,537
 28 FILING DATE: 24-Aug-2001
 29 CLASSIFICATION: <Unknown>
 30
 31 PRIOR APPLICATION DATA:
 32 APPLICATION NUMBER: 08/284,391
 33 FILING DATE: 02-AUG-1994
 34 APPLICATION NUMBER: 08/195,395
 35 FILING DATE: 14-FEB-1994
 36 APPLICATION NUMBER: 07/847,566
 37 FILING DATE: 06-MAR-1992
 38 APPLICATION NUMBER: 07/665,961
 39 FILING DATE: 07-MAR-1991
 40 ATTORNEY/AGENT INFORMATION:
 41 NAME: Elbing, Karen L
 42 REGISTRATION NUMBER: 35,238
 43 REFERENCE/DOCKET NUMBER: 00786/247001
 44 TELECOMMUNICATION INFORMATION:
 45 TELEPHONE: 617-428-0200
 46 TELEFAX: 617-428-7045
 47 TELEX: <Unknown>
 48
 49 INFORMATION FOR SEQ ID NO: 29:
 50 SEQUENCE CHARACTERISTICS:
 51 LENGTH: 398 amino acids
 52 TYPE: amino acid
 53 STRANDEDNESS: single
 54 TOPOLOGY: linear
 55
 56 MOLECULE TYPE: protein
 57 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 58 MS-09-939-537-29

Query Match	78.1%;	Score 1029;	DB 10;	Length 398;
Best Local Similarity	100.0%;	Pred. No. 9.7e-74;		
Matches 200;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	MNRGVEFRHLILVLOALALPATQGNKVVLGGKGYTELCTASOKSIOPHMNSNQIK	60
Db	1	MNRGVEFRHLILVLOALALPATQGNKVVLGGKGYTELCTASOKSIOPHMNSNQIK	60
Qy	61	ILGNQGSFLTKGSPSKLNRADRSRLMDQGNFPLIKLKIEDSDTYICEVEDQKEEYOL	120
Db	61	ILGNQGSFLTKGSPSKLNRADRSRLMDQGNFPLIKLKIEDSDTYICEVEDQKEEYOL	120
Qy	121	LVNGLTANSDTHLLOQSILTLLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDSG	180
Db	121	LVNGLTANSDTHLLOQSILTLLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDSG	180
Qy	181	TWTCIVLONOKVEFEKIDIV	200
Db	181	TWTCIVLONOKVEFEKIDIV	200

RESULT 9

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US-10-097-044A-1
; Sequence 1, Application US/10097044A
; Publication No. US20030143220A1
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/097,044A
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250765
FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-044A-1

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Query Match	78.1%;	Score 1029;	DB 14;	Length 402;
Best Local Similarity	100.0%;	Pred. No. 9.8e-74;		

Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
DB 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
QY 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
QY 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
```

RESULT 10

US-09-891-119A-9
Sequence 9, Application US/09891119A
Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 457
TYPE: PRT
ORGANISM: human
US-09-891-119A-9

Query Match 78.1%; Score 1029; DB 11; Length 457;
Best Local Similarity 100.0%; Pred. No. 1,2e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
DB 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
QY 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
QY 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
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RESULT 11

US-09-939-537-5
Sequence 5, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian

Banapour, Babak
Romeo, Charles
Kolanus, Waldemar

TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elding LLP
STREET: 176 Federal Street

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-AUG-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-939-537-5

Query Match 78.1%; Score 1029; DB 10; Length 462;
Best Local Similarity 100.0%; Pred. No. 1,2e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
DB 1 MNRGVPFRHLILVQLALPAATQGNKVVLGKGGTVELTCTASQKSIQFHMKNNOIK 60
    |||
QY 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
DB 61 ILGNQGSFLTGKPSKLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
    |||
QY 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
DB 121 LVFGLTANSDBTHLLOQGSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
    |||
QY 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
DB 181 TWTCTVLQNKQKVEFKIDIV 200
    |||
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RESULT 12

US-09-243-008-5
Sequence 5, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:

APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular Immunity by

Receptor Chimeras

NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street


```
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
/ SOFTWARE: Wordperfect (Version 5.0)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/243.008
/ FILING DATE: 02-Feb-1999
/
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US/08/394.176
/ FILING DATE: SEPTEMBER 11, 1995
/ APPLICATION NUMBER: 08/203,866
/ FILING DATE: February 28, 1994
/ APPLICATION NUMBER: 07/847,566
/ FILING DATE: March 6, 1992
/ APPLICATION NUMBER: 07/665,961
/ FILING DATE: March 7, 1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Karen F. Lech, Ph.D
/ REGISTRATION NUMBER: 35,238
/ REFERENCE/DOCKET NUMBER: 00786/270001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 462 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-243-008-5

Query Match      78.1%; Score 1029; DB 11; Length 462;
Best Local Similarity 100.0%; Pred. No. 1,2e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/
/ 181 TWTCTVLONQKKVEFKIDIV 200
/ 181 TWTCTVLONQKKVEFKIDIV 200
/ 181 TWTCTVLONQKKVEFKIDIV 200
/
/ RESULT 13
/ US-09-939-537-6
/ Sequence 6, Application US/09939537
/ Publication No. US20030138410A1
/ GENERAL INFORMATION:
/ APPLICANT: Seed, Brian
/ Banapour, Babak
/ Romeo, Charles
/ Kojanec, Waldemar
/ TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
/ CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Clark & Elbing LLP
```

```
/ STREET: 176 Federal Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/939.537
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 08/284,391
/ FILING DATE: 02-AUG-1994
/ APPLICATION NUMBER: 08/195,395
/ FILING DATE: 14-FEB-1994
/ APPLICATION NUMBER: 07/847,566
/ FILING DATE: 06-MAR-1992
/ APPLICATION NUMBER: 07/665,961
/ FILING DATE: 07-MAR-1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Elbing, Karen L.
/ REGISTRATION NUMBER: 35,238
/ REFERENCE/DOCKET NUMBER: 00786/247001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-428-0200
/ TELEFAX: 617-428-7045
/
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 532 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-537-6

Query Match      78.1%; Score 1029; DB 10; Length 532;
Best Local Similarity 100.0%; Pred. No. 1,4e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/ 1 MNRGVFPHLLVLTGLALLPAATQGNKVVLGKGGDTVELTCTASQKSIQPFHKNQIK 60
/
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/ 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEEYOL 120
/
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/ 121 LVFGLTANSDDTHLLQGQSLLTLTLESPGSSPSVQCRSPRGKNIQSGKTLVSQLELDQSG 180
/
/ 181 TWTCTVLONQKKVEFKIDIV 200
/ 181 TWTCTVLONQKKVEFKIDIV 200
/ 181 TWTCTVLONQKKVEFKIDIV 200
/
/ RESULT 14
/ US-09-243-008-6
/ Sequence 6, Application US/09243008
/ Publication No. US20040005334A1
/ GENERAL INFORMATION:
/ APPLICANT: Seed, Brian et al.
/ Receptor Chimeras
/ TITLE OF INVENTION: Redirection of Cellular Immunity by
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson P.C.
```

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,008
FILING DATE: 02-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11, 1995
APPLICATION NUMBER: 08/203,866
FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-243-008-6
Query Match 78.1%; Score 1029; DB 11; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
DB 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
QY 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQKQKVEFKIDIV 200
DB 181 TWTCTVLOQKQKVEFKIDIV 200
RESULT 15
US-09-939-537-4
Sequence 4, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
Kojanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
NUMBER OF SEQUENCES: 53
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Clark & Ebling LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Eibing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-537-4
Query Match 78.1%; Score 1029; DB 10; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
DB 1 MNRGVPFRHLILVQLALPAPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNOIK 60
QY 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
DB 61 ILNGGSEFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
QY 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGILTANSDTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQKQKVEFKIDIV 200
DB 181 TWTCTVLOQKQKVEFKIDIV 200
RESULT 16
US-09-243-008-4
Sequence 4, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular Immunity by
NUMBER OF SEQUENCES: 40
Receptor Chimeras
CORRESPONDENCE ADDRESSES:

```
/ ADDRESS: Fish & Richardson P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
/ SOFTWARE: Wordperfect (Version 5.0)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/243,008
/ FILING DATE: 02-Feb-1999
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US/08/394,176
/ FILING DATE: SEPTEMBER 11,1995
/ APPLICATION NUMBER: 08/203,866
/ FILING DATE: February 28, 1994
/ APPLICATION NUMBER: 07/847,566
/ FILING DATE: March 6, 1992
/ APPLICATION NUMBER: 07/665,961
/ FILING DATE: March 7, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Karen F. Lech, Ph.D
/ REGISTRATION NUMBER: 35,238
/ REFERENCE/DOCKET NUMBER: 00786/270001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 575 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-243-008-4

Query Match      78.1%; Score 1029; DB 11; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
DB      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
QY      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
DB      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
QY      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
DB      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
QY      181  TWTCTVLONQKKVEFKIDIV 200
      181  TWTCTVLONQKKVEFKIDIV 200
DB      181  TWTCTVLONQKKVEFKIDIV 200

RESULT 17
US-10-151-274-3
/ Sequence 3, Application US/10151274
/ Publication No. US20030064071A1
/ GENERAL INFORMATION:
/ APPLICANT: Litzman, Dan R.
/ APPLICANT: Kwon, Douglas S.
/ APPLICANT: van Kooyk, Yvette
/ APPLICANT: Geilendeck, Theo
/ TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
/ TITLE OF INVENTION: INTO
/ TITLE OF INVENTION: CELLS
```

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/ FILE REFERENCE: 1049-1-017
/ CURRENT APPLICATION NUMBER: US/10/151,274
/ CURRENT FILING DATE: 2002-05-20
/ PRIOR APPLICATION NUMBER: US/09/517,605
/ PRIOR FILING DATE: 2000-03-02
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 3
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-151-274-3

Query Match      77.7%; Score 1023; DB 12; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
DB      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
QY      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
DB      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
QY      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
DB      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
QY      181  TWTCTVLONQKKVEFKIDIV 200
      181  TWTCTVLONQKKVEFKIDIV 200
DB      181  TWTCTVLONQKKVEFKIDIV 200
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RESULT 18
US-10-103-597A-39
/ Sequence 39, Application US/10103597A
/ Publication No. US20030096432A1
/ GENERAL INFORMATION:
/ APPLICANT: Jakobsen, Bent Karsten
/ TITLE OF INVENTION: Screening Methods
/ FILE REFERENCE: 102286.142
/ CURRENT APPLICATION NUMBER: US/10/103,597A
/ CURRENT FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: PCT/GB00/03579
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: GB 9922352.1
/ PRIOR FILING DATE: 1999-09-21
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO: 39
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-597A-39

Query Match      77.7%; Score 1023; DB 14; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
DB      1  MNRGVPRHLLLVQLALPPATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNSQIK 60
QY      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
DB      61  ILNGGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKLIKIEDSDTYICEVEDQKEEYQL 120
QY      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
DB      121  LVFGILTANSDTHLLOQGSLLTLESPPSSPVOCRSRPGKNIQGGKTLVSQLELDQSG 180
QY      181  TWTCTVLONQKKVEFKIDIV 200
      181  TWTCTVLONQKKVEFKIDIV 200
DB      181  TWTCTVLONQKKVEFKIDIV 200
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Db      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
RESULT 19
US-10-188-444-39
; Sequence 39, Application US/10188444
; Publication No. US20030104635A1
; GENERAL INFORMATION:
; APPLICANT: Jakobson, Bent Karsten
; TITLE OF INVENTION: Screening Methods
; FILE REFERENCE: 102286.142 (CIP)
; CURRENT APPLICATION NUMBER: US/10/188,444
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: PCT/GB00/03579
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: GB 9922352.1
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-444-39

Query Match      77.7%; Score 1023; DB 14; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Qy      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Db      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Qy      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Db      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Qy      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db      181 TWCTVVLQNKVKVEFKIDIV 200
|||||

RESULT 20
US-10-207-655-170
; Sequence 170, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-170

Query Match      77.7%; Score 1023; DB 14; Length 458;
Best Local Similarity 99.5%; Pred. No. 3.5e-73;
Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Qy      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Db      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Qy      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
```

```
Qy      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Db      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Qy      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Db      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Qy      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db      181 TWCTVVLQNKVKVEFKIDIV 200
|||||

RESULT 21
US-08-681-219-27
; Sequence 27, Application US/08681219
; Publication No. US20020058607A1
; GENERAL INFORMATION:
; APPLICANT: Takaaki Sato and Junn Yanagisawa
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLOF
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-27

Query Match      77.5%; Score 1021; DB 8; Length 458;
Best Local Similarity 99.0%; Pred. No. 5e-73;
Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Db      1 1NRGVPRHLLVLQALLPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60
|||||
Qy      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Db      61 ILGNQGSFLTKGSPKLNDRADSRSLMDQGNFPLIIKLIKEDSDTYICEVEDQKEEVQL 120
|||||
Qy      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Db      121 LVFGLTNSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
|||||
Qy      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
Db      181 TWCTVVLQNKVKVEFKIDIV 200
|||||
```

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 22

US-09-230-111C-25
; Sequence 25, Application US/09230111C
; Publication No. US20030203414A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; APPLICANT: Yanagisawa, Junn
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
; SIGNAL-TRANSDUCING PROTEINS AND THE GLOF (PDZ/DHR)
; TITLE OF INVENTION: DOMAIN AND USES THEREOF
; FILE REFERENCE: 48962-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,111C
; CURRENT FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 458
; TYPE: PRT
; ORGANISM: human
US-09-230-111C-25

Query Match 77.5%; Score 1021; DB 11; Length 458;

Best Local Similarity 99.0%; Pred. No. 5e-73;

Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 23

US-10-092-138-25
; Sequence 25, Application US/10092138
; Publication No. US20030170723A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT APPLICATION NUMBER: US/10/092,138
; CURRENT FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 458
; TYPE: PRT
; ORGANISM: human
US-10-092-138-25

Query Match 77.5%; Score 1021; DB 14; Length 458;

Best Local Similarity 99.0%; Pred. No. 5e-73;

Matches 198; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 24

US-09-891-119A-2
; Sequence 2, Application US/09891119A
; Publication No. US20040013683A1
; GENERAL INFORMATION:
; APPLICANT: Madden, Paul J.
; TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
; FILE REFERENCE: 24577-CY-B
; CURRENT APPLICATION NUMBER: US/09/891,119A
; CURRENT FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Human
US-09-891-119A-2

Query Match 76.8%; Score 1012; DB 11; Length 397;

Best Local Similarity 98.5%; Pred. No. 2.2e-72;

Matches 197; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Db 1 MNRGVPFRHLVLVQLALPPAATQGNKVVLGKKGDTVELTCTASQKSIQFHMKNNOIK 60

Qy 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Db 61 ILGNQSSFLTKGPSKLNDRADSRSLMDQGNFPLIIKMLKIEDSDTYICEVEDQKEEVQL 120

Qy 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Db 121 LVFGLTANSPTHLLQGOSLTITLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELDQSG 180

Qy 181 TWCTVLOKQKVEFKIDIV 200

Db 181 TWCTVLOKQKVEFKIDIV 200

RESULT 25

US-10-024-329-32
; Sequence 32, Application US/10024329
; Publication No. US20030157063A1
; GENERAL INFORMATION:
; APPLICANT: SANHADJI, Kamel
; APPLICANT: TOURAINE, Jean-Louis
; APPLICANT: LEROY, Pierre
; APPLICANT: MEHTALI, Majid
; TITLE OF INVENTION: Gene therapy using anti-gp41 antibody and cd4 immunoadhesin
; FILE REFERENCE: 109993
; CURRENT APPLICATION NUMBER: US/10/024,329
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 448
; TYPE: PRT
; ORGANISM: human scd4
US-10-024-329-32

Query Match 69.7%; Score 917.5; DB 14; Length 448;
Best Local Similarity 95.5%; Pred. No. 8.7e-65;
Matches 191; Conservative 0; Mismatches 2; Indels 7; Gaps 6;

QY 1 MNRGVPFRLHLVLTALIPATQGNKVLGKGGTVELTCTASQKSIQPHMKNNOIK 60
DB 1 MNRGVPF-HLLVLTALIPATQGNKVLGKGGTVELTCTASQKSIQPHMKNNOIK 59
QY 61 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQL 120
DB 60 ILGNQGSFLTKGPSKLNDRADSRSLMDQGNFPLIINKLIEDSDTYIC--VDQKEEVQL 117
QY 121 LVFGJLTANSDFHLLQGQSLTTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 118 LVFGJLTANSDFHLLQGQSLTTLTLESPPGSSPSVQCRSPR-KNI-QGKTLVS-LQLDQSG 174
QY 181 TWTCTVLQNKVKVERKIDIV 200
DB 175 TWTCTVLQNKVKVERKIDIV 193

RESULT 26
US-10-097-044A-4
; Sequence 4, Application US/10097044A
; Publication No. US20030143220A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,044A
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9681
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 434 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-097-044A-4
Query Match 69.6%; Score 916; DB 14; Length 434;
Best Local Similarity 100.0%; Pred. No. 1.1e-64;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QGNKVLGKKGGDTVELTCTASQKSIQPHMKNNOIKILGNQGSFLTKGPSKLNDRADSR 83
DB 56 QGNKVLGKKGGDTVELTCTASQKSIQPHMKNNOIKILGNQGSFLTKGPSKLNDRADSR 115
QY 84 RSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVFGJLTANSDFHLLQGQSLTTL 143
DB 116 RSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVFGJLTANSDFHLLQGQSLTTL 175
QY 144 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLQNKVKVERKIDIV 200
DB 176 ESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLQNKVKVERKIDIV 232

RESULT 27
US-10-073-118-26
; Sequence 26, Application US/10073118
; Publication No. US2003005454A1
; GENERAL INFORMATION:
; APPLICANT: BECOUART, JEROME
; TITLE OF INVENTION: ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS
; FILE REFERENCE: 06832.1429-03
; CURRENT APPLICATION NUMBER: US/10/073,118
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 09/551,635
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/004,319
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 08/479,146
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/295,078
; PRIOR FILING DATE: 1994-08-26
; PRIOR APPLICATION NUMBER: 08/121,236
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 07/955,243
; PRIOR FILING DATE: 1992-10-01
; PRIOR APPLICATION NUMBER: 07/561,879
; PRIOR FILING DATE: 1990-08-02
; PRIOR APPLICATION NUMBER: FR 89 10480
; PRIOR FILING DATE: 1989-08-03
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 788
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein fusion
; OTHER INFORMATION: Prepro-HSA-V1V2
US-10-073-118-26
Query Match 68.6%; Score 903; DB 14; Length 788;
Best Local Similarity 95.7%; Pred. No. 2.6e-63;
Matches 178; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 19 LPAAQG---NKVLGKKGGDTVELTCTASQKSIQPHMKNNOIKILGNQGSFLTKGPS 74
DB 599 LVAASQALGLKVVVLGKGGDTVELTCTASQKSIQPHMKNNOIKILGNQGSFLTKGPS 658
QY 75 KLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVFGJLTANSDFHLL 134
DB 659 KLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVQLVFGJLTANSDFHLL 718
QY 135 QGQSLTTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLQNKVKVE 194
DB 719 QGQSLTTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLQNKVKVE 778
QY 195 FKIDIV 200

Db 779 FKIDIV 784

```
RESULT 28
US-09-934-060A-26
; Sequence 26, Application US/09934060A
; Patent No. US20020155121A1
; GENERAL INFORMATION:
; APPLICANT: Devico, Anthony L.
; APPLICANT: Fouts, Timothy R.
; APPLICANT: Tuskan, Robert G.
; TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
; FILE REFERENCE: 4115-144 CIP
; CURRENT APPLICATION NUMBER: US/09/934,060A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/684,026
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,321
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized construct
US-09-934-060A-26
```

```
Query Match      68.3%; Score 899; DB 9; Length 178;
Best Local Similarity 100.0%; Pred. No. 8,1e-64;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 86
    |||||
DB 2 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 61

QY 87 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 146
    |||||
DB 62 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 121

QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 200
    |||||
DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 175
```

```
RESULT 29
US-09-759-841-6
; Sequence 6, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manousos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000664.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-6
```

Query Match 68.3%; Score 899; DB 9; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 27 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 86
    |||||
DB 2 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 61

QY 87 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 146
    |||||
DB 62 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 121

QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 200
    |||||
DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 175
```

```
RESULT 30
US-09-934-060A-13
; Sequence 13, Application US/09934060A
; Patent No. US20020155121A1
; GENERAL INFORMATION:
; APPLICANT: Devico, Anthony L.
; APPLICANT: Fouts, Timothy R.
; APPLICANT: Tuskan, Robert G.
; TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
; FILE REFERENCE: 4115-144 CIP
; CURRENT APPLICATION NUMBER: US/09/934,060A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/684,026
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/158,321
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized construct
; NAME/KEY: MISC FEATURE
; LOCATION: (586)..(586)
; OTHER INFORMATION: Xaa can be any amino acid
; NAME/KEY: MISC FEATURE
; LOCATION: (589)..(589)
; OTHER INFORMATION: Xaa can be any amino acid
US-09-934-060A-13
```

Query Match 68.3%; Score 899; DB 9; Length 590;
Best Local Similarity 100.0%; Pred. No. 3.7e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 27 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 86
    |||||
DB 399 KVLGKGGDTVELTCTASOKKSIQPHMKNQKIKILNGSGFLTKGPKLNDRADSRSL 458

QY 87 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 146
    |||||
DB 459 WDOGNFPLIIKLIKIEDSDTYICEVEDQKEEVQLVFGILTANSDTHLLQGOSLTLTLESP 518

QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 200
    |||||
DB 519 PSSSPVQCRSPRGKNIQGGKTLVSQLELDGSGTCTVNLONQKVEFKIDIV 572
```

```
RESULT 31
US-09-934-060A-2
; Sequence 2, Application US/09934060A
; Patent No. US20020155121A1
; GENERAL INFORMATION:
; APPLICANT: Devico, Anthony L.
; APPLICANT: Fouts, Timothy R.
```

```
APPLICANT: Tuskan, Robert G.
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
FILE REFERENCE: 4115-144 CIP
CURRENT APPLICATION NUMBER: US/09/934,060A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 720
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized construct
NAME/KEY: MISC_FEATURE
LOCATION: (716)..(716)
OTHER INFORMATION: Xaa can be any amino acid
NAME/KEY: MISC_FEATURE
LOCATION: (719)..(719)
OTHER INFORMATION: Xaa can be any amino acid
US-09-934-060A-2
```

```
Query Match      68.3%; Score 899; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,8e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 27 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPKSLNDRADSRSL 86
DB 529 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPKSLNDRADSRSL 588
QY 87 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDTHLLQGOSLTLTLESP 146
DB 589 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDTHLLQGOSLTLTLESP 648
QY 147 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLOKQKVEFKIDIV 200
DB 649 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLOKQKVEFKIDIV 702
```

```
RESULT 32
US-09-934-060A-4
Sequence 4, Application US/09934060A
Patent No. US20020155121A1
GENERAL INFORMATION:
APPLICANT: Devito, Anthony L.
APPLICANT: Fouts, Timothy R.
APPLICANT: Tuskan, Robert G.
TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND METHODS OF USE
FILE REFERENCE: 4115-144 CIP
CURRENT APPLICATION NUMBER: US/09/934,060A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/684,026
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/158,321
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 720
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized construct
NAME/KEY: MISC_FEATURE
LOCATION: (716)..(716)
OTHER INFORMATION: Xaa can be any amino acid
NAME/KEY: MISC_FEATURE
LOCATION: (719)..(719)
OTHER INFORMATION: Xaa can be any amino acid
US-09-934-060A-4
```

```
Query Match      68.3%; Score 899; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 4,8e-63;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 27 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPKSLNDRADSRSL 86
DB 529 KVLGKGGDTVELTCTASQKKSIOFHWNKSNQIKILNQGSFLTKGPKSLNDRADSRSL 588
QY 87 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDTHLLQGOSLTLTLESP 146
DB 589 WDGNFPLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDTHLLQGOSLTLTLESP 648
QY 147 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLOKQKVEFKIDIV 200
DB 649 PGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSGTWTCTVLOKQKVEFKIDIV 702
```

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RESULT 33
US-10-024-329-33
Sequence 33, Application US/10024329
Publication No. US20030157063A1
```

```
GENERAL INFORMATION:
APPLICANT: SANHADJI, Kamel
APPLICANT: TOURAINE, Jean-Louis
APPLICANT: LEROY, Pierre
APPLICANT: MEHTALI, Majid
TITLE OF INVENTION: Gene therapy using anti-gp41 antibody and cd4 immunoadhesin
FILE REFERENCE: 109993
CURRENT APPLICATION NUMBER: US/10/024,329
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 184
TYPE: PRT
ORGANISM: L, D1, J1, D2 domains of human bCD4
US-10-024-329-33
```

```
Query Match      66.9%; Score 881; DB 14; Length 184;
Best Local Similarity 95.3%; Pred. No. 2,3e-62;
Matches 181; Conservative 1; Mismatches 2; Indels 6; Gaps 5;
```

```
QY 1 MNRGVPRHLLVQLALLPAAQGNKVLGKGGDTVELTCTASQKKSIOFHWNKSNQIK 60
DB 1 MNRGVPR-HLLLVQLALLPAAQGNKVLGKGGDTVELTCTASQKKSIOFHWNKSNQIK 59
QY 61 ILNQGSFLTKGPKSLNDRADSRSLWDGNFPLIKNLKIEDSDTYICEVEDQKEVQL 120
DB 60 ILNQGSFLTKGPKSLNDRADSRSLWDGNFPLIKNLKIEDSDTYICEVEDQKEVQL 117
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 118 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPR-KNI-GGKTLVS-LELDQSG 174
QY 181 TWCTCTVLOKQ 190
DB 175 TWCTCTVLOKQ 184
```

```
RESULT 34
US-09-891-119A-10
Sequence 10, Application US/09891119A
Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
```


LENGTH: 94
TYPE: PRT
ORGANISM: human
US-09-891-119A-10

Query Match 37.5%; Score 494; DB 11; Length 94;
Best Local Similarity 100.0%; Pred. No. 7e-32;

Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 QGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILNGSFLTKGPKLNDPDR 83
DB 1 QGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILNGSFLTKGPKLNDPDR 60
QY 84 RSLMDGNFPLIINKLKIEDSDTYICEVEDKKE 117
DB 61 RSLMDGNFPLIINKLKIEDSDTYICEVEDKKE 94

RESULT 35
US-10-105-545-26

Sequence 26, Application US/10105545
Publication No. US20030144479A1

GENERAL INFORMATION:

APPLICANT: Mark, Greene I.

APPLICANT: William, William V.

APPLICANT: Weiner, David B.

APPLICANT: Cohen, Jeffrey A.

APPLICANT: Kleber-Bemons, Thomas

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

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APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

APPLICANT: Williams, Robert M.

QY 77 NDRADRSRLMDGNFPLIINKLKIEDSDTYIC 109
DB 61 NDRADRSRLMDGNFPLIINKLKIEDSDTYIC 93

RESULT 36
US-10-125-692-10

Sequence 10, Application US/10125692
Publication No. US20030044429A1

GENERAL INFORMATION:

APPLICANT: Adem, Alan

APPLICANT: Hayashi, Fumitaka

APPLICANT: Smith, Kelly D.

APPLICANT: Underhill, David M.

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

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APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

APPLICANT: Ozinsky, Adrian

Query Match 36.1%; Score 475; DB 14; Length 612;
Best Local Similarity 52.8%; Pred. No. 2.5e-29;
Matches 104; Conservative 32; Mismatches 55; Indels 6; Gaps 5;

QY 1 MNRGVPFH-LLVLQALLPAAQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOI 59
DB 1 MCRATSLRLLLLQLLSQLAVTQKTLVKGEGESALPCESQKTIPTFWFSDQR 60
QY 60 KILNGG-SFLTKG-PEKLNDRADRSRLMDGNFPLIINKLKIEDSDTYICEVEDKE 116
DB 61 KILNGG-SFLTKG-PEKLNDRADRSRLMDGNFPLIINKLKIEDSDTYICEVEDKE 119
QY 117 EVOLVFLGTANSPTHLQGSLLTLES-PGSSPSVQCPKRNIGGKTLVSQLE 175
DB 120 EVELWVFTVTPSGISLQGSLLTLESNSKVSINPLTECHGKGVSSKVLMSNLR 179
QY 176 LODSGTWTCTVLQNGK 192
DB 180 VQSDSFNCTVTLQDK 196

RESULT 37
US-09-135-238B-8

Sequence 8, Application US/09135238B
Patent No. US2002017565A1

GENERAL INFORMATION:

APPLICANT: No. US2002017565A1, Garry P.

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

APPLICANT: Hitoishi, Yasumichi

QY 17 ALPAAQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILNGSFLTKGPKSL 76
DB 1 ALPAAQGNKVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILNGSFLTKGPKSL 60


```
US-10-105-545-25
; Sequence 25, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffery A.
; APPLICANT: Kieher-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USI
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/11492US2
; CURRENT APPLICATION NUMBER: US/10/105,545
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-105-545-25

Query Match          18.1%; Score 238; DB 14; Length 95;
Best Local Similarity 54.3%; Pred. No. 1.8e-11;
Matches 51; Conservative 14; Mismatches 25; Indels 4; Gaps 3;

QY      19 LPAATGKRVVIGKKDYTELTCTASQKSTIQFHWKNSQIKILNQG-SFLTKG--PSK 75
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      3 LLAVTGKTLVIGKEGSAELPCSSQKKITVTFWTFSDQRKILGQHGKGVLRGGSPSQ 62
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      76 LNDRADRSRLMDQGNFPLIINKLKTEDSDTYIC 109
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      63 F-DRPDSKKGAWKGSFPLINKLKTEDSDTYIC 95
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 41
US-10-076-674-4
; Sequence 4, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
```

```
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-4

Query Match          11.4%; Score 150; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64 NQGSFLTKGSPSKLNDRADRSRLMDQGN 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      22 NQGSFLTKGSPSKLNDRADRSRLMDQGN 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 42
US-10-076-674-5
; Sequence 5, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-5

Query Match          11.4%; Score 150; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64 NQGSFLTKGSPSKLNDRADRSRLMDQGN 91
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      22 NQGSFLTKGSPSKLNDRADRSRLMDQGN 49
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 43
US-10-355-161A-4
; Sequence 4, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-4

Query Match          11.4%; Score 150; DB 15; Length 50;
```

Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 NOGSFLTGPSTKLNDRADSRSLMDQGN 91
DB 22 NOGSFLTGPSTKLNDRADSRSLMDQGN 49

RESULT 44
US-10-355-161A-5

; Sequence 5, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)_(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-5

Query Match 11.4%; Score 150; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 NOGSFLTGPSTKLNDRADSRSLMDQGN 91
DB 22 NOGSFLTGPSTKLNDRADSRSLMDQGN 49

RESULT 45
US-10-311-823-13

; Sequence 13, Application US/10311823
; Publication No. US20040116683A1
; GENERAL INFORMATION:
; APPLICANT: Bryan J. Boyle
; APPLICANT: Nancy Mize
; APPLICANT: Matthew Arterburn
; APPLICANT: Y. Tom Tang
; APPLICANT: George Yeung
; APPLICANT: Ping Zhou
; APPLICANT: Chenghua Liu
; APPLICANT: Vinod Asundi
; APPLICANT: Radoje T. Drmanac
; APPLICANT: Meng-Yun Wang
; APPLICANT: Lichuan Chen
; APPLICANT: Yea-Huey Yang
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTREMIMIN-LIKE
; FILE REFERENCE: HYS-17CIP/US
; CURRENT APPLICATION NUMBER: US/10/311,823
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US01/03651
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/632,085
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-311-823-13

Query Match 10.6%; Score 139; DB 16; Length 570;
Best Local Similarity 26.3%; Pred. No. 0.014;
Matches 56; Conservative 33; Mismatches 82; Indels 42; Gaps 9;

QY 4 GVPFRHLIVLQALLPAATQGNKVLGKKGD-----TWELTCRASQKKSIGFHWKNSNQ 58
DB 99 GVPFKSIRVDVQYLDPEPLTV-HQTVSDVRGNFYQKTEVFLRCTVSNPPARFTWKGSQ 157
QY 59 IKIANGOSFLTGPSTKLNDRADSRSLMDQGNPPLI-IRKLKTEDSPDYICEVEDQKE- 116
DB 158 -----TSHSQDNG-VDIYEPLTYQGETVKLKLRLRPQDYASTYQVSVRNVC 205
QY 117 --EVQLVFGLTANSDFHLQGGSLTVLTSPGSSPSVQC-----R 156
DB 206 GIPDKAITFRLTNTTAPPAK-LSVNETLVVNGENVTQCLLTGDPPLPQLQMSHGPGP 264
QY 157 SPRGNIQGKTLSSVQLQELQDSCTWTCTVLQN 189
DB 265 LPLGALQGG-TLSISPVQARDSGYNCATNN 296

RESULT 46
US-10-311-823-7

; Sequence 7, Application US/10311823
; Publication No. US20040116683A1
; GENERAL INFORMATION:
; APPLICANT: Bryan J. Boyle
; APPLICANT: Nancy Mize
; APPLICANT: Matthew Arterburn
; APPLICANT: Y. Tom Tang
; APPLICANT: George Yeung
; APPLICANT: Ping Zhou
; APPLICANT: Chenghua Liu
; APPLICANT: Vinod Asundi
; APPLICANT: Radoje T. Drmanac
; APPLICANT: Meng-Yun Wang
; APPLICANT: Lichuan Chen
; APPLICANT: Yea-Huey Yang
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTREMIMIN-LIKE
; FILE REFERENCE: HYS-17CIP/US
; CURRENT APPLICATION NUMBER: US/10/311,823
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US01/03651
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/632,085
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-311-823-7

Query Match 10.6%; Score 139; DB 16; Length 586;
Best Local Similarity 26.3%; Pred. No. 0.015;
Matches 56; Conservative 33; Mismatches 82; Indels 42; Gaps 9;

QY 4 GVPFRHLIVLQALLPAATQGNKVLGKKGD-----TWELTCRASQKKSIGFHWKNSNQ 58
DB 115 GVPFKSIRVDVQYLDPEPLTV-HQTVSDVRGNFYQKTEVFLRCTVSNPPARFTWKGSQ 173

QY 59 IKILNQSFLTQPSKLNDRADSRSLMDQGNFPLI-IKNLIKIEDSDTYICEVEDOKE- 116
 DB 174 -----FLSHQDNG-VDIYEPITYQGETKYLKKNLRPODYASYTCQVSRVANC 221
 QY 117 --EVQLLVGLTANSPTHLIQGSLTLTLSPGSSPSVQC-----R 156
 DB 222 GIPDKAITRLTWTTPALPK-LSVNETLVNNGENVTVQCLLTGDPPLQLQWHSHPGP 280
 QY 157 SPRGKNIQGGKTLTSVQLELQDGTCTVTLQN 189
 DB 281 LPLGALAQGS-TLSTPSVQARDSGYNNCTATNN 312

RESULT 47

US-10-108-260A-4247
 ; Sequence 4247, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20040005560A1a1 full length cdna
 ; FILE REFERENCE: H1-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 4247
 ; LENGTH: 535
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-108-260A-4247

Query Match 10.1%; Score 133; DB 15; Length 535;
 Best Local Similarity 21.2%; Pred. No. 0.039; Indels 98; Gaps 13;

Matches 69; Conservative 49; Mismatches 110; Indels 98; Gaps 13;
 QY 1 MNRGVPFRHLVLQ-LALPAAATQGNKVLGKKDGTVELTCTAS--QKKSIOFHM-- 53
 DB 1 MDTGLWVFLVGLLRVQSVLVESSGGV--QPTSLRLSSASAGFFRHSAMVWVRQ 58
 QY 54 ---KSNQIKILNQSFLTQPS--KLNDRADSRSLMDQGNFPLI-IKNLIKIEDSDTY 107
 DB 59 AEGKLEWVGLIMNDSHXYGDSVGRFTISRDNRRM----FYIQMNSLKVEDTATY 113
 QY 108 ICEVE-----DQKEVOLVGLTANSPTHLIQGSLTLTLSPGSSPSVQCSPRG 160
 DB 114 YCAKEADNCRIDGHEMMRCLADKQGSDDVDVWGQGITVTVSTASTGSPSVFLAPCS 173
 QY 161 KNIQGS-----KTLSSVS-----OLELQDNG----- 180
 DB 174 RSTSGTALAGCLVKDYPPPEPVYSWNSGALTSCHTTPFAVLQSSGLYLSLSVTVVPSSS 233
 QY 181 ---TWTCV-----LQNKVVEFKIDI-----VPRASALPAPPGSALPDPOTA 221
 DB 234 LGTQTYTCVNNHKSNTKYDKVELKTPPLGDTHTTCPRCPPEKSCDTPPCRCPEPKSC 293
 QY 222 SALP-----DPPASALPA 235
 DB 294 DTPPCRCPEPKSCDTPPCRCPCA 319

RESULT 48

US-10-274-583-20
 ; Sequence 20, Application US/10274583
 ; Publication No. US20030138431A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Exelixis, Inc.
 ; TITLE OF INVENTION: LARCAPS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 ; FILE REFERENCE: EX02-119C
 ; CURRENT APPLICATION NUMBER: US/10/274,583
 ; CURRENT FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: 60/338,733
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: 60/357,600

; PRIOR FILING DATE: 2002-02-15
 ; PRIOR APPLICATION NUMBER: 60/361,196
 ; PRIOR FILING DATE: 2002-03-01
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 20
 ; LENGTH: 1477
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-274-583-20

Query Match 10.0%; Score 131.5; DB 14; Length 1477;
 Best Local Similarity 26.5%; Pred. No. 0.19;

Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9;

QY 34 GDTVELTCTASQKSIQFHMKNISNOIKILNQSFLTQPSKLNDRADSRSLMDQGNF 93
 DB 260 GNTVYFTCRABGNPKPEIIMLRNN-----NELSMKTDSSRLNLDGDT-- 301
 QY 94 LIIKLIKIEDSDTYICEV-----EDQKEVOLVGLTAN-----SDTHLQGSLLTL 141
 DB 302 LMIQNTQETDQGIYQCAKNVAGEVKTQSVTLRTFGSPARPTFYIQPONTVEVLGSEVTL 361
 QY 142 ----TLSPGSSPSVQCRSP-----RGKNIQGGKTLTSVQLELQDGTCTVTLQNKVY 193
 DB 362 ECSATGHPPRISWTRGRTPLPVDPRVNIPTSGGLYIQNVQDGSSEYACASATNNIDSV 421
 QY 194 EFKIDIVPRASALP--APPGSALPDPOT---ASALPDPPASA 232
 DB 422 HATAFTI--VQALPQFTVTPQDRVIVEGQTVDFQCEAKGNPPVYA 465

RESULT 49

US-10-231-956A-325
 ; Sequence 325, Application US/10231956A
 ; Publication No. US20040053233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lorens, James B.
 ; APPLICANT: Xu, Weiduan
 ; APPLICANT: Bogenberger, Jakob
 ; APPLICANT: Holland, Sacha
 ; APPLICANT: Rigel Pharmaceuticals, Incorporated
 ; TITLE OF INVENTION: Modulators of Angiogenesis
 ; FILE REFERENCE: 021044-004100US
 ; CURRENT APPLICATION NUMBER: US/10/231,956A
 ; NUMBER OF SEQ ID NOS: 522
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 325
 ; LENGTH: 1479
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-231-956A-325

Query Match 10.0%; Score 131.5; DB 12; Length 1479;
 Best Local Similarity 26.5%; Pred. No. 0.19;

Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9;

QY 34 GDTVELTCTASQKSIQFHMKNISNOIKILNQSFLTQPSKLNDRADSRSLMDQGNF 93
 DB 260 GNTVYFTCRABGNPKPEIIMLRNN-----NELSMKTDSSRLNLDGDT-- 301
 QY 94 LIIKLIKIEDSDTYICEV-----EDQKEVOLVGLTAN-----SDTHLQGSLLTL 141
 DB 302 LMIQNTQETDQGIYQCAKNVAGEVKTQSVTLRTFGSPARPTFYIQPONTVEVLGSEVTL 361
 QY 142 ----TLSPGSSPSVQCRSP-----RGKNIQGGKTLTSVQLELQDGTCTVTLQNKVY 193
 DB 362 ECSATGHPPRISWTRGRTPLPVDPRVNIPTSGGLYIQNVQDGSSEYACASATNNIDSV 421
 QY 194 EFKIDIVPRASALP--APPGSALPDPOT---ASALPDPPASA 232
 DB 422 HATAFTI--VQALPQFTVTPQDRVIVEGQTVDFQCEAKGNPPVYA 465

```

RESULT 50
US-10-211-462-87
; Sequence 87, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1496
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-211-462-87

```

```

Query Match 10.0%; Score 131.5; DB 15; Length 1496;
Beat Local Similarity 26.5%; Pred. No. 0.19;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9

Oy 34 GDVLELTCTTASOKKSIQPHMKNSNOIKILGNQGSFLTKGPSKLNDRADSRSLMDQGNFP 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 GNTVYFTCRABGNPKPEELIWLRRNN-----NELSMKTSRLNLDDGT-- 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 94 LIINKLKIEDSDTYICEV-----EDQKEVOLLVGLTAN-----SDTHLLOQSLLT 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 LMIQNTQRTDQGIYQCMKKNVAGEVKTQEVTLRYGSPARPFTVIQPNTEVLVGESVTL 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 142 -----TLSEPPGSSPSVQCRSP-----RGKNIQGGKTLVSQLELDSSGTWTCTVLONOKKY 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 ECSATGHPPRPRISWTRGRDTPLPVDPVRNVIIPSGGLYIQNVVQGSSEGCASATNNIDSV 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 194 EFKIDIVPRASALP---APPTGSALPDPQT---ASALPDPAPASA 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 HATAFII--VQALPQFTVTPQDRVIVIEGQTVDFQCEAKGNPPPVIA 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 53
US-10-276-774-1957
; Sequence 1957, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO: 1957
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1957

Query Match 10.0%; Score 131.5; DB 12; Length 1498;
Beat Local Similarity 26.5%; Pred. No. 0.19;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9

Oy 34 GDVLELTCTTASOKKSIQPHMKNSNOIKILGNQGSFLTKGPSKLNDRADSRSLMDQGNFP 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 GNTVYFTCRABGNPKPEELIWLRRNN-----NELSMKTSRLNLDDGT-- 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 94 LIINKLKIEDSDTYICEV-----EDQKEVOLLVGLTAN-----SDTHLLOQSLLT 141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 LMIQNTQRTDQGIYQCMKKNVAGEVKTQEVTLRYGSPARPFTVIQPNTEVLVGESVTL 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 142 -----TLSEPPGSSPSVQCRSP-----RGKNIQGGKTLVSQLELDSSGTWTCTVLONOKKY 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 ECSATGHPPRPRISWTRGRDTPLPVDPVRNVIIPSGGLYIQNVVQGSSEGCASATNNIDSV 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 194 EFKIDIVPRASALP---APPTGSALPDPQT---ASALPDPAPASA 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 HATAFII--VQALPQFTVTPQDRVIVIEGQTVDFQCEAKGNPPPVIA 482
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 54
US-10-243-552-899
; Sequence 899, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y, Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei

```

```

APPLICANT: Weng, Gezhi
APPLICANT: Ma, Yundong
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: Polypeptides
CURRENT APPLICATION NUMBER: US/10/243,552
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/322,511
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
Remaining SEQ ID Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 998
SOFTWARE: pt_fl_genes Version 5.0
SEQ ID NO 899
LENGTH: 1498
TYPE: PRT
ORGANISM: Homo sapiens
US-10-243-552-899

Query Match 10.0%; Score 131.5; DB 12; Length 1498;
Best Local Similarity 26.5%; Pred. No. 0.19;
Matches 60; Conservative 27; Mismatches 92; Indels 47; Gaps 9.

Cy 34 GDTVELCTGSQKKSIGFHMWNSNQIILGNQGSFLTRKPSKILNDRADRSRLWDQGNFP 93
Db 277 GNTVYFTCRABGNKPETIMLRN-----NELSMKTDLSRLNLDDGT-- 318
Cy 94 LIINKLIEDSDYICEV-----EDQKEVOLVFGLTAN-----SDTHLQGSITL 141
Db 319 LMIQNTGETOGIGIQCAKNAVAGSVKIQEVLIRFGSPARTFVIGQNTREVLVGSVTL 378
Cy 142 ----TLESPPGSSPSVQCRSP---RGKNTIQGKTLVSQLELDSGTMTCTVLIQONKV 193
Db 379 ECSATGHPPIPSIWTRDRTPLPVDPRVNIIPSSGLYIQNVQGDSEYACSATNIDSV 438
Cy 194 EFKIDIVPRASALP---APPTGSALPPPQT---ASALPPPPASA 232
Db 439 HATVFII-VQALPQFTVTPQDRVIVIGQIVDFQCEAKGNPPVIA 482

RESULT 55
US-10-311-823-16
Sequence 16, Application US/10311823
Publication No. US2004011683A1
GENERAL INFORMATION:
APPLICANT: Bryan J. Boyle
APPLICANT: Nancy Mize
APPLICANT: Matthew Arterburn
APPLICANT: Y. Tom Tang
APPLICANT: George Yeung
APPLICANT: Ping Zhou
APPLICANT: Chenshua Liu
APPLICANT: Vinod Asundi
APPLICANT: Radoje T. Drmanac
APPLICANT: Meng-Yun Wang
APPLICANT: Lichuan Chen

```

```
/ APPLICANT: Yea-Huey Yang
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
/ FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
/ FILE REFERENCE: HYS-17CIP/US
/ CURRENT FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: PCT/US01/03651
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/632,085
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 374
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-311-823-16
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```
Query Match          9.9%; Score 131; DB 16; Length 374;
Best Local Similarity 27.3%; Pred. No. 0.036;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;
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QY 36 TVELCTASQKKSIOFHKMKNQIKILGNQGSFLTKPSKUNDRADRSRLMDQGNFPLI 95
DB 55 TVFLRCTVNSNPPARFTWKRGSD-----TLSSHQDNG-VDIYEPLYTQGETKVL 102
QY 96 -IKNLKIEDSDTYICEVEDQKE---EVQLVFGLTANSPTHLAQGSLLTLESPPGSSP 151
DB 103 KKLNLRPQDASYTCQSVRVNCGIPDKAITFRLTNTTAPPAALK-LSVNETLVNPGENV 161
QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELDQSGTWTCTVLON 189
DB 162 TVQCLLTGSDPLPOLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGYVNCATANN 216
```

```
RESULT 56
US-10-311-823-12
/ Sequence 12, Application US/10311823
/ Publication No. US20040116683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bryan J. Boyle
/ APPLICANT: Nancy Mize
/ APPLICANT: Matthew Arterburn
/ APPLICANT: Y. Tom Tang
/ APPLICANT: George Yeung
/ APPLICANT: Ping Zhou
/ APPLICANT: Chenghua Liu
/ APPLICANT: Vinod Asundi
/ APPLICANT: Radoje T. Drmanac
/ APPLICANT: Meng-Yun Wang
/ APPLICANT: Yea-Huey Yang
/ APPLICANT: Lichuan Chen
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
/ FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
/ FILE REFERENCE: HYS-17CIP/US
/ CURRENT FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: PCT/US01/03651
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/632,085
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 442
```

```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-311-823-12
```

```
Query Match          9.9%; Score 131; DB 16; Length 442;
Best Local Similarity 27.3%; Pred. No. 0.044;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;
```

```
QY 36 TVELCTASQKKSIOFHKMKNQIKILGNQGSFLTKPSKUNDRADRSRLMDQGNFPLI 95
DB 136 TVFLRCTVNSNPPARFTWKRGSD-----TLSSHQDNG-VDIYEPLYTQGETKVL 183
QY 96 -IKNLKIEDSDTYICEVEDQKE---EVQLVFGLTANSPTHLAQGSLLTLESPPGSSP 151
DB 184 KKLNLRPQDASYTCQSVRVNCGIPDKAITFRLTNTTAPPAALK-LSVNETLVNPGENV 242
QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELDQSGTWTCTVLON 189
DB 243 TVQCLLTGSDPLPOLQWSHGPGPLPLGALAQGG-TLSIPSVQARDSGYVNCATANN 297
```

```
RESULT 57
US-10-311-823-4
/ Sequence 4, Application US/10311823
/ Publication No. US20040116683A1
/ GENERAL INFORMATION:
/ APPLICANT: Bryan J. Boyle
/ APPLICANT: Nancy Mize
/ APPLICANT: Matthew Arterburn
/ APPLICANT: Y. Tom Tang
/ APPLICANT: George Yeung
/ APPLICANT: Ping Zhou
/ APPLICANT: Chenghua Liu
/ APPLICANT: Vinod Asundi
/ APPLICANT: Radoje T. Drmanac
/ APPLICANT: Meng-Yun Wang
/ APPLICANT: Lichuan Chen
/ APPLICANT: Yea-Huey Yang
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NEUROTROPIC-LIKE
/ FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
/ FILE REFERENCE: HYS-17CIP/US
/ CURRENT FILING DATE: 2003-09-29
/ PRIOR APPLICATION NUMBER: PCT/US01/03651
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 09/632,085
/ PRIOR FILING DATE: 2000-08-02
/ PRIOR APPLICATION NUMBER: 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-311-823-4

Query Match          9.9%; Score 131; DB 16; Length 458;
Best Local Similarity 27.3%; Pred. No. 0.046;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;
```



```

Db      259 TVQGLLTGGDDPLPQLQWMSHGPGRLPLGALAAQG--TLISIPSVQAARDSGYNNCTATTN 313

RESULT 58
US-10-024-918-27
; Sequence 27, Application US/10024918
; Publication No. US20020168718A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey
APPLICANT: Schense, Jason
APPLICANT: Zisch, Andreas
APPLICANT: Hall, Heike
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP
CURRENT APPLICATION NUMBER: US/10/024,918
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 1260
TYPE: PRT
ORGANISM: Mus Musculus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (516T..(604)
OTHER INFORMATION: the sixth Ig-like domain of the cell adhesion molecule LI
US-10-024-918-27

Query Match          9.9%; Score 131; DB 13; Length 1260;
Beet Local Similarity 23.9%; Pred.No.0.17; 95; Indels 50; Gaps 9;
Matches 56; Conservative 33; Mismatches 9;

Cy       10 LLLVLQLALLPAATOGKNVVLGKGDPVELTCTASQKSIO--FHWKNSNQIKILNGQS 67
           |||         ||| : | : | | | | | : | : |
Db        507 ILANLQVEAGDTITQGPRAIEKKARVTFTQASDPLQASITWRGR----- 557

Cy       68 FLTGPSKLNDRADSRSLMDGNFPFLIKNLEIDSDTYIC--EVEDQKEVOLVF 123
           |||||   ||| : | : | - - - - - |||||
Db        558 -----DLQEGRDSDKFYIEDGK-LVIQSLDSPQGVNCVASTELDVESRAQLTV 608

Cy       124 GLTN-----SDTHLLOQGS.LTLETSPSSPSVQCNSP-----RGNKIQGKTL 169
           |||     ||| ||| : | : | | : | : |
Db        609 GPSGEVPHILELSDRHLKQSQVHLSW----SPADHNSPIEKXDIEFDKEMAEKWPF 662

Cy       170 SVSDELQDSGTWTCTVLQNQKVE--FKDIVPRASALAPPPTGSALPDPOTA 221
           || : | : | ||| : | : | | : | : |
Db        663 SLGRY----PNQGTSTTLKLSPYHYTFRVTAINKTGPEPPSVSESVTPPEAA 712

RESULT 59
US-10-650-509-27
; Sequence 27, Application US/10650509
; Publication No. US20040082513A1
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey
APPLICANT: Schense, Jason
APPLICANT: Zisch, Andreas
APPLICANT: Hall, Heike
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
FILE REFERENCE: CIT 2606 CIP CON
CURRENT APPLICATION NUMBER: US/10/650,509
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: 10/024,918
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/057,052
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: PCT/US98/06617
PRIOR FILING DATE: 1998-04-02
PRIOR APPLICATION NUMBER: 60/042,143
PRIOR FILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.1

```

```

; LENGTH: 1260
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (516)..(604)
; OTHER INFORMATION: the sixth Ig-like domain of the cell adhesion molecule L1
US-10-650-509-27

Query Match          9.9%; Score 131; DB 16; Length 1260;
Best Local Similarity 23.9%; Pred. No. 0.17;
Matches    56; Conservative   33; Mismatches   95; Indels    50; Gaps     9;

QY      10 LLIVQLALLPATQGNKVVLGKKGDTVELTCTASQCKSIQ--FHWKNSNOKILIGNQS 67
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      507 ILANIQVKETATITQPFRSAIEKKGARVPTCOASFPSLQASITWRDGR----- 557

QY      68 FLTGPSKINDRSDRSRLMDQGNFPLIKNLKIEDSDTYIC----FEVDKEEVQLLVF 123
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      558 -----DLQEGDSDKFYIEDGK--LVISLDYSDDGNYSQVASTELDEVESRAQLLV 608
               |::||::||::||::||::||::||::||::||::||::||::||::||:

QY      124 GLTN-----SDTHLLQGQSLTLTLSPSGSSPVSVCORSP-----RGKNIGQSKTL 169
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
DB      609 GSFGVPFHLELDRIHLKKSQVHLSW-----SPAHDHNPSEIKYEIDFEDEKMAPKMF 662
               |::||::||::||::||::||::||::||::||::||::||::||::||:

QY      170 SVSQLELDQSGTWTCVTVLQNQKVE--FKDIVPRASALPAAPPGSALPDPOTA 221
       :|::||::||::||::||::||::||::||::||::||::||::||::||:
DB      663 SIGKV---PGNQSTSTLKLPVHYHTFVTAINKYGPGEPPSVSESIVTPEAA 712
               |::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 60
US-10-094-886-52
; Sequence 52, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patkurajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangoli, Esha
; APPLICANT: Gusev, Vladimír
; APPLICANT: Smithson, Glendina
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
; APPLICANT: Rascelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: LaRochele, William
; APPLICANT: Zhong, Wei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17

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; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 52
; LENGTH: 1315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-52

Query Match          9.9%; Score 131; DB 15; Length 1315;
Best Local Similarity 27.3%; Pred. No. 0.18;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY 36 TVELTCTASQKKSIOFHWKNSNQIKILGNQGSFLTKGPKSKNDRADSRRLMDQGNFPLI 95
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 152 TVFLRCTVNSNPAPRFWKRGSD-----TLSHQDNG-VDIYEPLYTGSETKVL 199
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 96 -IKNLIKEDSDPTVCEVEDQKE---EVQLVFGLTANSDTHLLOGQSITLTLESPPGSSP 151
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 200 KTKNLRPQDYASVTCQVSVRVNCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV 258
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELQDSGTWCTVLQN 189
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 259 TVQCLLTGSDPLPQLQWSHGPGPLPLGALAQGG-TLSISVQARDSGYINCTATNN 313
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 61
US-10-094-886-38
; Sequence 38, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernyev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patlurejan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Gorman, Linda
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Miller, Charles
; APPLICANT: Casman, Stacie
; APPLICANT: Pena, Carol
; APPLICANT: Gangolli, Bsha
; APPLICANT: Gusev, Vladimir
; APPLICANT: Smithson, Glenda
; APPLICANT: Zeinusen, Bryan
; APPLICANT: Gerlach, Valerie
; APPLICANT: Pochart, Pascal
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard
```

```

; APPLICANT: Raetelli, Luca
; APPLICANT: Spaderina, Steven
; APPLICANT: Labochelle, William
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-290 B
; CURRENT APPLICATION NUMBER: US/10/094,886
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,182
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/288,052
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/318,510
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/314,018
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/274,849
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/296,693
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/313,626
; PRIOR FILING DATE: 2001-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 38
; LENGTH: 1386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-886-38

Query Match          9.9%; Score 131; DB 15; Length 1386;
Best Local Similarity 27.3%; Pred. No. 0.19;
Matches 48; Conservative 25; Mismatches 67; Indels 36; Gaps 7;

QY 36 TVELTCTASQKKSIOFHWKNSNQIKILGNQGSFLTKGPKSKNDRADSRRLMDQGNFPLI 95
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 152 TVFLRCTVNSNPAPRFWKRGSD-----TLSHQDNG-VDIYEPLYTGSETKVL 199
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 96 -IKNLIKEDSDPTVCEVEDQKE---EVQLVFGLTANSDTHLLOGQSITLTLESPPGSSP 151
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 200 KTKNLRPQDYASVTCQVSVRVNCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV 258
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 152 SVQC-----RSPRGKNIQGGKTLVSQLELQDSGTWCTVLQN 189
    |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB 259 TVQCLLTGSDPLPQLQWSHGPGPLPLGALAQGG-TLSISVQARDSGYINCTATNN 313
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 62
US-09-808-602-69
; Sequence 69, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020155115A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
```

```

PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-808-602-69

Query Match          9.8%; Score 129; DB 9; Length 338;
Best Local Similarity 23.2%; Pred. No. 0.045;
Matches    57; Conservative   40; Mismatches     91; Indels      58; Gaps       11

QY      10 LLLVLTQLALLPAA-----TQGKRVVLGGKGDTVELTTASQKKSIQTFFHKNSNQIKI 61
DB      14 LVLRRLCLLPTGLPVRSVDNFNRGTNDITVRGDDTAIRCVLEEDKNS-KVAWLNRRSGILF 72
QY      62 LGNGGSFLTKGPSKUNDRA--DSRSLMDQGNFPPLINKLKIEDSDTYICEVEDQKE--- 116
DB      73 AGHD-----KMSLDPRVELEKRHSL----EYSRIQGVADYDGGSYTCVSOTGHEPKT 121
QY      117 -EVOLLVG-----LTNSTDHLLLOQSILTLPLESPPSSPSVOQR-SPRKNIGGKT- 168
DB      122 SGVVLIIVVPKRMISISSDYVNESANTLVCMANGREBPVTWMHLTPTGFEFGEEBY 181
QY      169 LSVSQELQDSGSTWTCTVLAQ-----NQKVPEKDIPV-----RA 203
DB      182 LEIDGITREGSKYECKAANEVSADVQVKATVANYPFTTESKSNEATTGRQAALKCEA 241
QY      204 SALRAP 209
DB      242 SAVAP 247

RESULT 63
US-09-800-198-58
Sequence 58, Application US/09800198
Publication No. US20030087816A1
GENERAL INFORMATION:
APPLICANT: Vernet, Cornile AM
APPLICANT: Fernandes, Elma
APPLICANT: Shmukets, Richard A
APPLICANT: Herrmann, John L
APPLICANT: Majumder, Kumud
APPLICANT: Mishra, Vishna
APPLICANT: Mezes, Peter S
APPLICANT: Raestelli, Luca
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-697
CURRENT APPLICATION NUMBER: US/09/800,198
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,596
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-198-58

Query Match          9.8%; Score 129; DB 10; Length 338;
Best Local Similarity 23.2%; Pred. No. 0.045;
Matches    57; Conservative   40; Mismatches     91; Indels      58; Gaps       11

QY      10 LLLVLTQLALLPAA-----TQGKRVVLGGKGDTVELTTASQKKSIQTFFHKNSNQIKI 61
DB      14 LVLRRLCLLPTGLPVRSVDNFNRGTNDITVRGDDTAIRCVLEEDKNS-KVAWLNRRSGILF 72
QY      62 LGNGGSFLTKGPSKUNDRA--DSRSLMDQGNFPPLINKLKIEDSDTYICEVEDQKE--- 116
DB      73 AGHD-----KMSLDPRVELEKRHSL----EYSRIQGVADYDGGSYTCVSOTGHEPKT 121
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Oy      117 -EVOLLVFG-----LTANSPTHTLLOQSLLTLTLESPGSSPEVQCR--SPGSKNIQGGKT- 168
Db      122 SÖYLLVQVPPKRNISNSSVYTNESGNTVLCVMANGRPPEPVTYRHLTPTGRFEGEGBEY 161
Oy      169 LVSQLELDQDSGTWCTVTLQ-----NOKKVEFKDIDV-----RA 2030
Db      182 LEILITGREGSGVCEKANEVSADYKQVKTATVVPPTINESKSNATGTGRQSLKCEA 2411
Oy      204 SALPAP 209
Db      242 SAVPAP 247

RESULT 64
US-10-042-865-92
; Sequence 92, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Basha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patuturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ference L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malysankar, Uriel M
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glennda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-865-92

Query Match      9.8%; Score 129; DB 12; Length 338;
Beet local Similarity 23.2%; Pred No. 0.045;

```



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Db      14 LVLVLGLCLLPTGLPVRSDVFNKRGDNTITVRQGDTHALIRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLANDRA--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKE--- 116
Db      73 AGHD-----KMSLDPRVELEKRNHSL-----EYSLRIQKVYDVBGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
Db      122 SQVYLIVQVPPKISNISSDVTNVEGSSVTLVCMANGRPPEVITWRHLTPLGREFGESEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVYTVNPTITTSKSNKNEATTGQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

```

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RESULT 67
US-09-808-602-72
; Sequence 72, Application US/09808602
; Patent No. US2002015515A1
; GENERAL INFORMATION:
; APPLICANT: Vermet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hezerman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015515A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-808-602-72

```

```

Query Match      9.6%; Score 126; DB 9; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

Qy      10 LVLVLGLCLLPPA-----TQGNKVVLGKKGDTVELTCTASQKSIQFHKNSNQIKI 61
Db      14 LVLRLCLLPLTCLPVRSDVFNKRGDNTITVRQGDTHALIRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLANDRA--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKE--- 116
Db      73 AGHD-----KMSLDPRVELEKRNHSL-----EYSLRIQKVYDVBGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
Db      122 SQVYLIVQVPPKISNISSDVTNVEGSSVTLVCMANGRPPEVITWRHLTPLGREFGESEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVYTVNPTITTSKSNKNEATTGQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

```

```

RESULT 68
US-09-800-198-61
; Sequence 61, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vermet, Corine AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Hezerman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-800-198-61

```

```

Query Match      9.6%; Score 126; DB 10; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

```

```

Qy      10 LVLVLGLCLLPPA-----TQGNKVVLGKKGDTVELTCTASQKSIQFHKNSNQIKI 61
Db      14 LVLRLCLLPLTCLPVRSDVFNKRGDNTITVRQGDTHALIRCVLEDKNS-KVAMLNRSGLIF 72
Qy      62 LQNGSFLTKGPSKLANDRA--DSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKE--- 116
Db      73 AGHD-----KMSLDPRVELEKRNHSL-----EYSLRIQKVYDVBGSYCSVQTOHEPKT 121
Qy      117 -EVQLLVFG---LTANSPTHLQGSLLTLESPPGSSPSVQCR--SPRGKNIQGGKT- 168
Db      122 SQVYLIVQVPPKISNISSDVTNVEGSSVTLVCMANGRPPEVITWRHLTPLGREFGESEY 181
Qy      169 LSVSOLELDQSGTWCTCTVQ-----NOKVPEFKIDIVP-----RA 203
Db      182 LEILGITRQSGKYECKKANEVSSADVQKVYTVNPTITTSKSNKNEATTGQASLKCEA 241
Qy      204 SALPAP 209
Db      242 SAVPAP 247

RESULT 69
US-10-042-865-91
; Sequence 91, Application US/10042865
; Publication No. US20040029216A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Li, Li
; APPLICANT: Zehrusen, Bryan D
; APPLICANT: Casman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patuturajan, Meera
; APPLICANT: Vermet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia

```

```

/ APPLICANT: Boldog, Ference L
/ APPLICANT: Grosse, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Macdougall, John
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, David
/ TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
/ FILE REFERENCE: 21402-537
/ CURRENT APPLICATION NUMBER: US/10/042,865
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/260,417
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/260,831
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/272,338
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/274,876
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/284,704
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 264
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 91
/ LENGTH: 338
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-042-865-91

Query Match          9.6%; Score 126; DB 12; Length 338;
Best Local Similarity 22.8%; Pred. No. 0.079;
Matches 56; Conservative 41; Mismatches 91; Indels 58; Gaps 11;

QY 10 LLLVLQALLPRA-----TQGNKVVLGKKGDIVELCTASQKKSIOFHMKNSNOIKI 61
DB 14 LVLRLRLCLPTGLPVRVSDFNRTGDNITVRQGDPAIRCVVEDKNS-KVAWLNSGITF 72
QY 62 LGNQGSLFKGSKLNDRA--DSRSLWDOGFPFLIKLKIEDSDTYICEVEDQKE--- 116
DB 73 AHD-----KMSLDPRVELEKRAL---EYSLRIQVNDVDEGSYTCVQTOHEKXT 121
QY 117 -EVQLLIVFG---LTANSDTHLLQGOSLTLTLESPPGSSPSVQCR--SPRGKNIQGKT- 168
DB 122 SQVYLIVQVPKISNIDVTNENGSNVTLCMANGRPPEVITWRHLFPLGRFGESEBY 181
QY 169 LSVQLELDSDSGTWCTVQ-----NOKVKEFKIDIVP-----RA 203
DB 182 LELILGTRGSKYECKANEVSDAVKQKVTVNVPPTITESKSENAITGRQASLKCEA 241
QY 204 SALPAP 209
DB 242 SAVPAP 247

RESULT 70
US-10-042-865-14
/ Sequence 14, Application US/10042865
/ Publication No. US20040029216A1
/ GENERAL INFORMATION:
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Li, Li
/ APPLICANT: Zehusen, Bryan D
/ APPLICANT: Casman, Stacie J
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Spytek, Kimberly
```

```

/ APPLICANT: Zhong, Mei
/ APPLICANT: Gangoli, Esha A
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Vernet, Corine A.M
/ APPLICANT: Taylor, Sarah
/ APPLICANT: Tchernev, Velizar T
/ APPLICANT: Miller, Charles E
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Boldog, Ference L
/ APPLICANT: Grosse, William M
/ APPLICANT: Alsobrook II, John P
/ APPLICANT: Gerlach, Valerie L
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Rothenberg, Mark E
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Macdougall, John
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, David
/ TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
/ FILE REFERENCE: 21402-537
/ CURRENT APPLICATION NUMBER: US/10/042,865
/ PRIOR FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: 60/260,417
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: 60/260,831
/ PRIOR FILING DATE: 2001-01-10
/ PRIOR APPLICATION NUMBER: 60/272,338
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/274,876
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/284,704
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 264
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-042-865-14

Query Match          9.6%; Score 126; DB 12; Length 354;
Best Local Similarity 23.0%; Pred. No. 0.083;
Matches 53; Conservative 37; Mismatches 92; Indels 48; Gaps 10;

QY 20 PAATQGNKVVLGKKGDIVELCTASQKKSIOFHMKNSNOIKILNQGSLFKGP-----SK 75
DB 41 PMAVNDMMV--RKGDPAADRLCYLEDGAS--KGAWLNSSTIFAG--GDKMSVDPRVLSIT 95
QY 76 LNDPADRSRLWDOGFPFLIKLKIEDSDTYICEVEDQKEEVLVFGTLTA----- 127
DB 96 LNKR-----DVSLOIQVNDVDDGTYTCVQTOHTPRYQVH-LTVQVPRXIYD 143
QY 128 -NSDTHLLQGOSLTLTLESPPGSSPSVQCR--SPRGKNIQCKTLTSVQLELDSDSGTWCT 184
DB 144 ISNDMTVNEGTNVTTLCLATGCKPEPSISWRHISPAKPFENGQGLDITGTLTRDQAGEYEC 203
QY 185 TV-----LQNKVKEFKIDIVPRASALPAPT-----GSALPDP 218
DB 204 SAENDVSPDVRAKVKVYNFAPFTIQELKSGVYTRGSGILRCBAGVPPP 253

RESULT 71
US-09-989-722-517
/ Sequence 517, Application US/09989722
/ Patent No. US20020072067A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
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CURRENT FILING DATE: 2001-11-19
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Db 212 GSSRPFMWQDSTSAEDTSPALSSGSSKPRVSIPIWRIILPVLVLISLSAALIIFC 268

RESULT 73
US-09-989-279-517
Sequence 517, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tyman, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PJC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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RESULT 74
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; APPLICANT: Ashkenazi, Avi J.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; PRIOR FILING DATE: 1998-05-07

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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match          9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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DB      65 OGSFLL--KGPSLNDRA---DSRSLSMOGNEPLIIKULKIEDSDTYCEVEDQKEEQ 119
      62 SGTIVAEESQETMKRVSIRDSRQEL---SLIVTLMLTLDDAGEYWCVEKRGPPDS 117
QY      120 LTVFGLTANSDFLLQGSITLTLLESPGSSPSVQCRSPRGKNIQCKTLVSQLE---- 175
      118 LLI-----SLVFPPGPC-----CPSPSPTFQ-----PLATTRLQPKAK 151
QY      176 -----LQDSGTCTCTVLQONQKVEFKIDIVPRASAL-----PA--PPT 211
      152 AQQTPPGTSPGLYPAATTAKGKGTAEXAPLPCTSOYGHERTSQYGTSPHPATSPPA 211
QY      212 GSALPPPO--TASALDPPASA-----LPAALAVISFLGLGLGVAC 252
DB      212 GSRPMPQDSTSAEDTSPALSSGSKPRVSIPIWRILAPVLVLSLSAAGLIAPC 268

RESULT 75
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/ Sequence 517, Application US/09989731
/ Patent No. US20020103125A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnovers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltzen, Mary E.
/ APPLICANT: Goddard, Audrey
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/ APPLICANT: Grimaldi, J. Christopher
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/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
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/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C70
/ CURRENT APPLICATION NUMBER: US/09/989,731
/ CURRENT FILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLIQIALLPV--ATQGNKVILGKKGDTVELTCTASOK-KSIOFMKNSNOIKIGN 64
DB 2 RLVLVWGCILLPVEALLEGEEISGFGDTVSLQCTYRELRHKKYCKKGGILPSCR 61
QY 65 QGSFLT--KGPSKINDRA---DSRRSLMDQNPFLIKNKIEDSDTYICEVDQKEBQ 119
DB 62 SGTIYAEEGQETKGVISIRDSRQEL---SLIVTLMNLTLDAGEYWCCEKRPDES 117
QY 120 LTVFGLTRANSDTHLQGOSSLTTLSPGSSPSYQCRSPRKNIQGGKTLVSQLE---- 175
DB 118 LLI-----SLFVFGGC-----CPSPSPYQ-----PLATTLQPPAK 151
QY 176 -----LDPSGTCTCTVLQNKKEVFKIDIVRASAL-----PA--PPT 211
DB 152 AQOTOPPELTSRGLYPATTAATKQGTGAERAPLGTQYGHERTSQYTGTSPPHATSPRA 211
QY 212 GSALPDPQ--TASALPPPPAASA-----LPAALAVISPLGLGLVAC 252
DB 212 GSRPPQLDSTSAEDTSALSSGSSKPRVSIPIWRIAPVLVILSLISAAGLIAFC 268

RESULT 76
US-09-989-732-517
Sequence 517, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivan J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19

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35 PRIOR FILING DATE: 1998-07-07
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37 PRIOR APPLICATION NUMBER: 60/091982
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41 PRIOR APPLICATION NUMBER: 60/092182
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43 PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13

[illegible]

RESULTS 77
US-09-991-073-517
Sequence 517, Application US/09991073/517
Patent No. US2002012576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Boctstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C15
CURRENT APPLICATION NUMBER: US/09/1991.073
CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09
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Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Pred. No. 0.092; Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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Qy 120 LIVFGLTNSDTHLQGGSLTLTLLESPPGSSBSVQCSRPKGNIOGKTLVSQLE---- 175
Db 118 LLI-----SLFVPPGPC-----CPSPSPTFQ-----PLATTRLQPRAX 151
Qy 176 -----LQBSGWTCTVNLQNKVEFKIDIVPRASAL-----PA--PPT 211
Db 152 AQQTQPPGLTSPGLYPAATTAKQGTGAAPPLPETSQYGHERTSQYGTGSPHPTSPPA 211
Qy 212 GSALPDPQ--TASALDPDPAASA-----DPAALAVISFLGLGLGVAC 252
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RESULT 78
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; Sequence 517, Application US/09990442
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Feron, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 9.5%; Score 125; DB 9; Length 332;
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Patent No. US20020137075A1
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Godowski, Paul J.
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APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C25
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RLHLVLQALLPA--ATGKNKVLGKKGDVLTCTASQK-KSIQFMKNSNQIKIGN 64

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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09
Query Match 9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;
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Db 2 RLVLVLMGCLLPGYEALEGGPEEISGFEQDVTSLQCTYREELRDHRTKWCRRKGLFSRC 61
Qy 65 QGSFLLT-KGSPKLDNRA---DSRSRLWQGNFPLIKNLKIEDSDTYICEVEDQKEEVO 119
Db 62 SGTIYAEEGQETMKGKRSINDSRGL-----SLITLNLNLTLQDAGEWCGEKXGPPDS 117
Qy 120 ILVFGILTANSDTHLLQGGSLTTLTSPSSPSVQCRSPRGNNIGGKTLVSQLE---- 175
Db 118 LLI-----SLFVPPGFC-----CPSPSPTFQ-----PLATTRLQPYAK 151
Qy 176 -----LQDSGTCTVNLQNKVEFKIDIVPPASAL-----PA--PPT 211
Db 152 AQQTQPPGLTSPGLYPAATTAKQKGTGABAPLPETSYGHERTSQYGTSPHPTSPPA 211
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RESULT 83
US-09-978-295A-216
; Sequence 216, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT APPLICATION NUMBER: US/09/978,295A
PRIOR APPLICATION NUMBER: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
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Query Match          9 5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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RESULT 84
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
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; APPLICANT: Pan, James
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; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVQLALLPA--ATQGNKVVLGKKGPVETCTASOK-KSIOFMKNSNQIKLGN 64
DB 2 RLVLVWGCLLPYELBEPFEISGFGDVISIQCTYRELRHKKRWCKGGLISRC 61
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DB 118 LLI-----SLFFPSPC-----CPSPSPRPQ-----PLATTLQPKAK 151
QY 176 -----LDSGWTCTVQONKKEFKIDIVRASAL-----PA--PPT 211
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QY 212 GSALPDPQ--TASALPPPPASA-----LPALAVISFLIGLGVAC 252
DB 212 GSSRPPLQDLBSTSADTSPLSSGSSKPRVSIPIWRLIAPVLVLSLSAAGLIAFC 268

RESULT 85
US-09-978-697-216
; Sequence 216, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Efron, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerltsen, Mary E.
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; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

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/ APPLICANT: Roy, Margaret Ann
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/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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Query Match 9.5%; Score 125; DB 9; Length 332;
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DB 62 SGTIAEEGGQETWKGKRVISIRDSQEL---SLIVLNLTLQDGEYWCVEKKGPDSS 117
QY 120 LVLVGLTANSDTHLQGGSLTLTLSPGSSPSVOCRSRPGKNIQGGKTLVSQLE--- 175
DB 118 LLI-----SLFVFPGPC-----CPSPSPFTQ-----PLATTRLQPRAX 151
QY 176 -----LQDSGTCTCTVQLQNKVVERKIDIVPPASAL-----PA--PPT 211
DB 152 AQQTPPGGLTSPGLYPAATTAKGTGAAPLPFGTSQYGHERTSQYTGTSPPHPTSPPA 211
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;; Sequence 517 Application US/09989293A

;; Patent No. US20020177164A1

;; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone

;; APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter

;; APPLICANT: Gerlitsen, Mary E.

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;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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RESULT 87
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; Patent No. US7002017553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
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APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
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APPLICANT: Gao, Wei-Qiang
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PRIOR APPLICATION NUMBER: 60/083558


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/ PRIOR FILING DATE: 1998-04-29
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
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Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Pred. No. 0.092; Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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QY 8 RHLLVLLQALALPA--ATQGNKVLGKGGDTVELTCTASOK-KSIQFHWKNSNQIKILGN 64
DB 2 RLVLVLMGCLLPBGVALLEGPEIISFEGDPTSLQCTYBELRDKHKYCRKGILFSC 61
QY 65 QGSEFLT-KPFSKLDNRA--DSRRSLMDQGNFLLIKULKIEDSDTYICEVEDOKEEVO 119
DB 62 SGTIVAEEGQETMKGRVSIKRSRQL---SLIVLWLVLTQDAEYWGCVGEKRGPDSS 117
QY 120 LTVFGLTASDTHLLOGQSLTLTLESPGSSPSVQCRSRGKNIOGKTLISVQLE---- 175
DB 118 LLI-----SLVFPGPC-----CPSPSPPTFQ-----PLATTRLQPKAK 151
QY 176 -----LQDSGTWTCVTLQNOKVTEFKIDIVRASAL-----PA--PPT 211
DB 152 AOOTGPGLTSPULYPAATTAKGKGALNPLPGISQYGHERTSQTGTSPHAPSPPA 211
QY 212 GSALPDPQ--TASALDPPAASA-----LPAALAVISFLLGLGIVAC 252
DB 212 GSSRPQMQLDSTSAEDTSPALSSGSSKPRVSIPIWVILAPVLVILSLSAAGLIAPC 268
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RESULT 88
US-09-999-832A-216
/ Sequence 216, Application US/09999832A
/ Publication No. US20020192706A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Baker Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan
/ APPLICANT: Ferrara, Napoleon
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerder, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C63
/ CURRENT APPLICATION NUMBER: US/09/999,832A
/ CURRENT FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
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/ PRIOR APPLICATION NUMBER: 60/077641
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/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079664
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3	PRIOR FILING DATE: 1998-03-27	
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11	PRIOR FILING DATE: 1998-03-30	
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21	PRIOR FILING DATE: 1998-03-31	
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4	PRIOR FILING DATE: 1998-04-29
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59	PRIOR APPLICATION NUMBER: 60/085697
60	PRIOR FILING DATE: 1998-05-15

Query Match 9.5%; Score 125; DB 9; Length 332;
 Best Local Similarity 22.9%; Pred. No. 0.092;
 Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLTGALLPA--ATQGNKVVVLGGKDPVELVETLASQK-KSIQPHMKNSSQIKLGN 64
 QY 2 RLVLVLMGCLLLPGVLEALEGPEEISGFECDVLSIQCTYRRELDHRYKRWCKRGKGLIPSRC 61
 Db 65 QQSFLT--KGSPKLANDRA---DSRRSLMDQSNFPLIINKLKIEDSDTYITVEVDQAEVQ 119
 QY 62 SGTVAAEEGQETMGKRVISIRDSROEL---SLVLTLMNLTLLDQAGYWCVGVERGPDES 117
 Db 120 LTVFGLTANSDTHLLKQGSGLTLLTESPPGSSPVQCRSPGKNIGQKGLTCSQLE---- 175
 QY 118 LVL-----SLVFPFGPC-----CPSPSPPTQ-----PLATTRLPDPAK 151

QY 176 -----LQDSGTCVTVLQONKVEFKIDIVRASAL-----PA--PPT 211
Db 152 AAOGTQPGILTSPELVYAATTAKQKGTGAEPPLPGTSQYGHERTSQTGTSPHPATSPPA 211
QY 212 GSALPDPO--TASALDPPAASA-----LPALAVISFLLGLGLGVAC 252
Db 212 GSSRPFQWQJDSSTASERTSPALSSGSSKPRVSIWVRIILAPVLVLISLSAAGLIANC 268

RESULT 89
US-09-989-735-517
Sequence 517, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimeidi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Pred. No. 0.092;

Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

8 RHLLVLAALPA--ATGKNVLTGKGDVLTCTTSQK-KSIQFHKNSNITKILGN 64

Db 2 RLVLWLCULLPGYEALEGBEISGFGDVTSLQCTYREBLDRHKYCKKGGILFSRC 61
Qy 65 QGSFLT--KQPSKXNDRA---DSRRSLMDQNFPLIKNKIEDSDTYICEVEDQKEBQ 119
Db 62 SGTIYAEBSGQETWKGVSRDSRQEL---SLVTIMNLTLDAGGYWCGVEKRGDEES 117
Qy 120 LVLVGLTRANSPTHLLOQSLSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLE---- 175
Db 118 LLI-----SLVFPPPC-----CPPSPPTFQ-----PLATRTLQPKAK 151
Qy 176 -----LQDSGWTCTVLQONQKVEFKIDYVRASAL-----PA--PPT 211
Db 152 AQCTPPGLTSPGIVPATTAKQGTGAEPPLPGTSQYGHERTQYGTGSPHATSPFA 211
Qy 212 GSALPDPQ--TASALPPPPASA-----LPAALAVISFLGLGLGVAC 252
Db 212 GSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPIWVRLAPVLVLSLSAAGLIAFC 268

RESULT 90

US-09-990-444-517
Sequence 517, Application US/09990444
Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyere, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Iyar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730P1C19

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28


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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      9.5%; Score 125; DB 9; Length 332;
Beet Local Similarity 22.9%; Pred. No. 0.092;
Matches    68; Conservative   38; Mismatches 109; Indels   82; Gaps   13

OY      RHLVLVQLALLPA--ATQGNKVYLGGKDDYTELTCTASQK-KSIQFHHKNSNOIKLGN 64
DB      2 RLVLVLMGCLLLPGYEALGEPEISGFEGEDTVSLCCTYNEELDRHKVKCRKGILFSRC 61
OY      QGSFLT--KGPEKLNDRA---DSRSLMDQGNEPLIKLKIEDSDTYICEVEDOKEEYQ 119
DB      62 SGTIAEERGQDTMGGRVISIRSRQEL-----SLVTIMNLTLDAGEYTCGYEKKGPDSS 117
OY      120 LVLFGSLTNSDTHLLQGOGLTLTTLESSPPGSSPVOCRSFRGNIGOGKTLVSOLE---- 175
DB      118 LLI-----SLVFVPGPC-----CPESPSTPFG-----PLATTRIQLPKAX 151
OY      176 -----LQDSGTTCITVLOKQKYVEFKIDIVPRASAI-----PA-PPT 211
DB      152 AQQTTPGGLTSBGLPAATTAKQKTGAEPPLPGRSGYGHERTSYGTSBPAPSPPA 211
OY      212 GSALDPDQ--TKSALDPDPASA-----LPALAVISFLILGLGVAC 252
DB      212 GSRPPMQDSTSADDTSPALSSGSKPRVSI.PMVRTLPALVILSLLSAAGLIAFC 268

RESULT 91
US-09-991-181-517
; Sequence 517, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC53
; CURRENT FILING DATE: US/09/991,181
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945

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PRIOR FILING DATE:	1998-02-25
PRIOR APPLICATION NUMBER:	60/0708910
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/0833222
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/0846000
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/0871060
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/0876070
PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/0875593
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PRIOR APPLICATION NUMBER:	60/0877538
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PRIOR FILING DATE:	1998-06-17

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37 PRIOR APPLICATION NUMBER: 60/092182
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39 PRIOR FILING DATE: 1998-07-09

Query Match	9.5%	Score 125;	DB 9;	Length 332;
Best Local Similarity	22.9%	Pred. No. 0.092;		
Matches	68;	Conservative	38;	Mismatches 109;
			Indels	82;
			Gaps	13

[illegible]

US-RSULT 93
US-09-990-436-517
Sequence 517, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botsstein, David
APPLICANT: Deanoeyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Geber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Andrew
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Yvar J.
APPLICANT: Nepler, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunnas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey

```

1 APPLICANT: Wood, William I.
2
3 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
4
5 TITLE OF INVENTION: Acids Encoding the Same
6
7 FILE REFERENCE: P2730PIC14
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9 CURRENT APPLICATION NUMBER: US/09/990,436
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11 CURRENT FILING DATE: 2001-11-14
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13 PRIOR APPLICATION NUMBER: 60/049787
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[illegible]

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14	PRIOR APPLICATION NUMBER: 60/0914787
15	PRIOR FILING DATE: 1998-07-02
16	PRIOR APPLICATION NUMBER: 60/0915444
17	PRIOR FILING DATE: 1998-07-01
18	PRIOR APPLICATION NUMBER: 60/0915191
19	PRIOR FILING DATE: 1998-07-02
20	PRIOR APPLICATION NUMBER: 60/0916266
21	PRIOR FILING DATE: 1998-07-02
22	PRIOR APPLICATION NUMBER: 60/0916333
23	PRIOR FILING DATE: 1998-07-02
24	PRIOR APPLICATION NUMBER: 60/0919787
25	PRIOR FILING DATE: 1998-07-07
26	PRIOR APPLICATION NUMBER: 60/0919822
27	PRIOR FILING DATE: 1998-07-07
28	PRIOR APPLICATION NUMBER: 60/0921822
29	PRIOR FILING DATE: 1998-07-09

Query Match	9.5%;	Score 125;	DB 9;	Length 332;
Best Local Similarity	22.9%;	Pred. No. 0.092;		
Matches	68;	Conservative	38;	Mismatches 109;
				Indels 82;
				Gaps 13.

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QY      RHLLVLTGLATLPA--AAGNCNVVLGKKGDVLTCTASQK-KSIIQFHKMSNOKILGN 64
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DB      2 RLIVLVLGMCILPEYEALEGPBEISGFEDVLSLCITREELDRHKRWCKKGGILSRSC 61
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QY      65 QGSFLT-KKPSKLDNDRA---DSRRSLMDGCFPLIINLKIETSDIYICEVEDOKEVQ 119
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::
DB      62 SGITVAEEQEGEMTKGKRVISIRDSQEL---SLIVTLNLTLDAGGEYMCVEKRPDES 117
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::
QY      120 LLYFGLTANSDTHLLQGSLLTILTESPGSSPSVQCRPRKNTQGGKITLSVSGLE--- 175
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DB      118 LLI-----SLFVFPGPC-----CPSPSPSTFQ-----PLATITLQPKAK 151
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QY      176 -----LQDSGTWTCVTLQNOQKVEFKDIVPRASAL-----PA--PPT 211
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DB      152 AAGTOPPGSLTSPELYPAATTAQKGTGAAPLPETSGYGHERTSQYGTGSPHATSPRA 211
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QY      212 GSAHPDQ--TASALDPAPASA-----LPALANVTSFLIGLGLVAC 252
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DB      212 GSSRPMPQDSTSAEDTSPALSSGSKKRPVSIIMVRIILAVLVILSLISAAGLIAFC 268
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US-09-993-687-517
 : Sequence 517, Application US/09993688
 : Publication No. US20020198149A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Ashkenazi, Avi J.
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eacott, Dan L.
 : APPLICANT: Ferrari, Napoleone
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gershenberg, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Goddard, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurev, Austin L.

```

; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C11
; CURRENT FILING DATE: US/09/1993, 687
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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/ PRIOR APPLICATION NUMBER: 60/091544
/ PRIOR FILING DATE: 1998-07-01
/ PRIOR APPLICATION NUMBER: 60/091519
/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091626
/ PRIOR FILING DATE: 1998-07-02
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/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09
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Query Match 9.5%; Score 125; DB 9; Length 332;

Best Local Similarity 22.9%; Pred. No. 0.092; Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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QY 8 RHLLVLQALALPA--ATOGNKVVLGKGDVTELTCTASQK-KSIOFHKNSNQIKLGN 64
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 2 RLVLVLMGGLLPGYALBEPETISGFEEDTVSLQCTYHELRDRHKWCKRGGLIFSRG 61
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 65 QGSFLL--KQPSKNDRA---DSRSLMDQGNFPLIIKNLKIEDSPTYICEVEDQKEVQ 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 62 SGTVAEEGQETMKGRVSIIRDSRQL---SLIVLMLNLTLDAGEYWCVEKKGPDDES 117
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 120 LTVFGTANSDFHLLQGGSLTTLTLESPPGSSPSVQCRSRGNKIQGKTLVSQLE--- 175
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 118 LLL-----SLFVFPFPC-----CPSPSPFPQ-----PLATTRLQPKAK 151
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 176 -----LQDSGTWTCTVLQONQKVEFKIDIVPRASAL-----PA--PPT 211
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 152 AQQTQPGTLSPGLYATTAATTAQKGTGAAPRLPGTSQYGHRTSQTYSPTSPHAPRA 211
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 212 GSALPFPQ--TASALPDPRAAS-----LPALAVISFLGLGLGVAC 252
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 212 GSSRPFWQDSTSAEDTSPALSSGSSKPRVSIIPWRIAPVLVLTSLLSAAGLIAFC 268
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RESULT 95

US-09-989-734-517
; Sequence 517, Application US/09989734
; Publication No. US2003003531A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc

```
/ APPLICANT: Eaton, Dan L.  
/ APPLICANT: Ferrara, Napoleone  
/ APPLICANT: Fong, Sherman  
/ APPLICANT: Gerber, Hanspeter  
/ APPLICANT: Geritsen, Mary E.  
/ APPLICANT: Goddard, Audrey  
/ APPLICANT: Godowski, Paul J.  
/ APPLICANT: Grimaldi, J. Christopher  
/ APPLICANT: Gurney, Austin L.  
/ APPLICANT: Kljavin, Ivar J.  
/ APPLICANT: Napier, Mary A.  
/ APPLICANT: Paoni, Nicholas F.  
/ APPLICANT: Roy, Margaret Ann  
/ APPLICANT: Stewart, Timothy A.  
/ APPLICANT: Tumas, Daniel  
/ APPLICANT: Watanabe, Colin K.  
/ APPLICANT: Williams, P. Mickey  
/ APPLICANT: Wood, William I.  
/ APPLICANT: Zhang, Zemin  
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
/ FILE REFERENCE: P2730P1C64  
/ CURRENT APPLICATION NUMBER: US/09/989, 734  
/ PRIOR FILING DATE: 2001-11-19  
/ PRIOR APPLICATION NUMBER: 60/049787  
/ PRIOR FILING DATE: 1997-06-16  
/ PRIOR APPLICATION NUMBER: 60/062250  
/ PRIOR FILING DATE: 1997-10-17  
/ PRIOR APPLICATION NUMBER: 60/065186  
/ PRIOR FILING DATE: 1997-11-12  
/ PRIOR APPLICATION NUMBER: 60/065311  
/ PRIOR FILING DATE: 1997-11-13  
/ PRIOR APPLICATION NUMBER: 60/066770  
/ PRIOR FILING DATE: 1997-11-24  
/ PRIOR APPLICATION NUMBER: 60/075945  
/ PRIOR FILING DATE: 1998-02-25  
/ PRIOR APPLICATION NUMBER: 60/078910  
/ PRIOR FILING DATE: 1998-03-20  
/ PRIOR APPLICATION NUMBER: 60/083322  
/ PRIOR FILING DATE: 1998-04-28  
/ PRIOR APPLICATION NUMBER: 60/084600  
/ PRIOR FILING DATE: 1998-05-07  
/ PRIOR APPLICATION NUMBER: 60/087106  
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/ PRIOR APPLICATION NUMBER: 60/088033  
/ PRIOR FILING DATE: 1998-06-04  
/ PRIOR APPLICATION NUMBER: 60/088326  
/ PRIOR FILING DATE: 1998-06-04  
/ PRIOR APPLICATION NUMBER: 60/088167  
/ PRIOR FILING DATE: 1998-06-05  
/ PRIOR APPLICATION NUMBER: 60/088202  
/ PRIOR FILING DATE: 1998-06-05
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RESULT 96
US-09-978-189-216
Sequence 216, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/083496

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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match          9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;
QY      8 RHLLVLQALLPA--ATGKNKVLGKGGDTVELTJTASOK-KSIQPHMKNSQIKILGN 64
DB      2 RLIVLWGLLLGAYALGEPREISGPEGDTVSLQCTYREELNDHKKYCRKGILFSRC 61
QY      65 QGSFLT--KQPSKLDNRA--DSRRSLMDQGNPLIITKNIKTEDSDTYICEVEDOKEEVQ 119
DB      62 SGTIVAEEGQETMKRQVSIKRSRQEL-----SLIVLWMLTLDDAETVCGVEKRPDDS 117
QY      120 LLVGLTANSDTHLLOGQSITLTLESPPGSSPSVQGRSPGKNIQGGKTLVSQGLE---- 175
DB      118 LLI-----SLVFPGPC-----CPPSPPTFQ-----PLATRLQPKAK 151
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QY      176 -----LQDSGTCTVLQNOQKVEFKIDIVPASAL-----PA--PPT 211
DB      152 AQTQPGGLTSPGLYPAATTAQCKTGAAPPLPCTSOYGHRTSQYCTSHRPAISPPA 211
QY      212 GSALPDPO--TASALPDPPASA-----LPALAVISFLIGLGVAC 252
DB      212 GSRPPMQLDSTASDTSABDTSPALSSGSSKPRVSIPIWRIIAPVLVLTLSAAGLIAFC 268

RESULT 97
US-09-997-653-517
; Sequence 517, Application US/0997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Geider, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: 60/088021
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

QY 8 RHLLVLTALPPA-ATQGNKVVVGKKGDTVELTCTASQK-KSIQFHWKSNQIKILGN 64
DB 2 RLVLVLMGCLLPVGEALGPEBISGEGDVTSLQCTYREIRDRHKRYKCRKGGILFGRRC 61

QY 65 OGSFLT--KGPSKLANDRA---DSRSLMDQGNPFLIIKNLKIETSDTYICEVEDEKEEYQ 119
DB 62 SGTIVAEERQETMKRQVSIROSRQEI---SLIVLWNTLTDABGEIWCGEKRPDSS 117
QY 120 LVLVFGTANSDFHLLQGOSLTLTLLESPGSSPEVQGRSPRGKNIQGGKTLVSQLE--- 175
DB 118 LVL-----SLVFPQPC-----CPSPSPFFQ-----PLATRLQPKAK 151
QY 176 -----LQDSCGTCTVLQONQKYEFKIDIVPRASAL-----PA--PPT 211
DB 152 AOGTQPPGLTSPFLYPAATTAKQKGTGAAPLPFGTSQYGHERTSQYTGSPHATSPPA 211
QY 212 GSALPDPQ--TASALDPPASA-----LPAALAVISFLGLGLGVAC 252
DB 212 GSRPFWQDSTSAEDTSPALSSGSKPRVSIPIWRIILAPVLVLSLSAAGLIARFC 268

RESULT 98
US-09-993-667-517
Sequence 517, Application US/09993667
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanoyere, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferreira, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Acidic Encoding and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993,667
PRIOR FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182

PRIOR FILING DATE: 1998-07-09
Query Match 9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;
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DB 2 RLVLVLMGCUILLPGYEALEGEPEISGFGEDIVSLQCTYRELRDHRKRYKCKRGKGLFGR 61
QY 65 QGSFLT--KQPSKANDRA--DSRRSLMDQNFPLIINKLIESDITYICEVEDQKEVQ 119
DB 62 SGITVAEEEGQETKKGRSIRDSROEL---SLIVTLWNLLODAGEYWCCEYKRGPD 117
QY 120 LLVFGLTANSDTHTLLOGSLTLTLSPGSSPSVQCSFPRKNIQGGKTLVLSOLE---- 175
DB 118 LLI-----SLFVPPGFC-----CPSPSPFTQ-----PLATTRLQPRAK 151
QY 176 -----LQSGTWTCTVLQNKQKVEFKIDIVRASAL-----PA--PPT 211
DB 152 AQOTQPPCLTSPGLYPATTAKQCKTGAEAPPLBGTSGYGHERTSQYTGTSPPHATSPDA 211
QY 212 GSALPDPQ--TASALPDPPASA-----LPAALAVISFLIGLGVAC 252
DB 212 GSSRPWQDSTSAEDTSPALSSGSKPRVSIPIWVRIAPVLVLSLSAAGLIAFC 268
RESULT 99
US-09-997-428-517
Sequence 517, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Ealon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/997,428
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match      9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

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      2 RLVLVLMGCLLPGEYALGPEISGFEDTVLSLQTYRELDHRKWKCRKGILFSRC 61
Qy      65 QGSFLT--KGPSKLNDR---DSRSLMDQGNFPLIKKLTIEDSDTYICEVEDQKEEYQ 119
      62 SGTIAEEGCGETMKGKRVSIKRSQRL-----SLIVTLMVLTQDAGEYWCVEKKGPDSS 117
Db      120 LIVFGITANSDFHLIQGSLTTLTLESPGSSPSVQCRSPRGNKIQGKTLVSQLE--- 175
      118 LLI-----SLVFEPGFC-----CPSPSPPTFQ-----PLATTRLQPKAK 151
Qy      176 -----LQDSGTCTCTVLQGNKKYEFKIDIVPASAL-----PA--PPT 211
      152 AQQTPPGSLTSPGLPAAATTAKGKTGAEPPLPGTSOYGHRTSQYGTSPHPTSPPA 211
Db      212 GSALPDPQ--TASALPDPPPASA-----LPALAVISFLGLGIVAC 252
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RESULT 100
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/ Sequence 517, Application US/09997666
/ Publication No. US20030027163A1
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerltsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2730P1C42
/ CURRENT APPLICATION NUMBER: US/09/997,666
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 9.5%; Score 125; DB 10; Length 332;
Best Local Similarity 22.9%; Pred. No. 0.092;
Matches 68; Conservative 38; Mismatches 109; Indels 82; Gaps 13;

Qy 8 RHLVLQALPA--ATQGNKVVVGKKDVTFTCTASOK-KSIOFHKNSNOIXIGN 64
Db 2 RLVLVLMGCLLPGEALGEPBEISGFGDIVSLCTYRELRDRKRYCKRGKGLFSRC 61
Qy 65 QGSFLT--KGPSKLDNRA---DSRSWLDQGNFPLINLKIEDSDTYICEVEDQKEVQ 119
Db 62 SGTIVAESEGQETMKGRVSRDSRQEL---SLVTLNWLTIQDAGEYWCVEKKGPDES 117
Qy 120 LTVFGLTANSSTHLQGGSLTTLTSPGSSPSVOCRRPGKNIGGKTLISVQLE---- 175
Db 118 LLI-----SLVFPGPC-----CPSPSPFTQ-----PLATTRLQPRAX 151
Qy 176 -----LQDSGTWTCTVLQONQKVEPKIDIVPPASAL-----PA--PPT 211
Db 152 AQOTPPGLTSPGLYPAATTKAGKTGAAPLPETSGYGHERTSQYGTSPHATSPFA 211
Qy 212 GSALPDPQ--TASALDPPASA-----LPAALAVISFLGLGLGVAC 252
Db 212 GSSRPWMQDLSRSDTSPALSSGSSKPRVSIWRIILAPVLVLSLSAAGLIAFC 268

Search completed: August 3, 2004, 13:47:49
Job time : 26.8374 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 3, 2004, 13:01:34 ; Search time 7.59249 Seconds

(without alignments)
1754.300 Million cell updates/sec

Title: SEQ6

Perfect score: 1117

Sequence: 1 MNRGVPRHLLVQLALP.....VISFLGLGVACVLRTR 258

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 125 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

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5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	78.8	310	3 US-08-477-4608-6	Sequence 6, Appli
2	1038	78.8	310	3 US-08-379-516-6	Sequence 6, Appli
3	1038	78.8	310	3 US-09-329-916-6	Sequence 6, Appli
4	1038	78.8	310	3 US-08-485-372A-6	Sequence 6, Appli
5	1038	78.8	310	4 US-09-409-006A-6	Sequence 6, Appli
6	1038	78.8	310	4 US-08-484-681-6	Sequence 6, Appli
7	1038	78.8	310	5 PCT-US93-07422-6	Sequence 6, Appli
8	1032.5	78.4	432	3 US-08-477-4608-2	Sequence 2, Appli
9	1032.5	78.4	432	3 US-08-379-516-2	Sequence 2, Appli
10	1032.5	78.4	432	3 US-09-329-916-2	Sequence 2, Appli
11	1032.5	78.4	432	3 US-08-485-372A-2	Sequence 2, Appli
12	1032.5	78.4	432	4 US-09-409-006A-2	Sequence 2, Appli
13	1032.5	78.4	432	4 US-08-484-681-2	Sequence 2, Appli
14	1032.5	78.4	432	5 PCT-US93-07422-2	Sequence 2, Appli
15	1030.5	78.2	530	3 US-08-477-4608-4	Sequence 4, Appli
16	1030.5	78.2	530	3 US-08-379-516-4	Sequence 4, Appli
17	1030.5	78.2	530	3 US-09-329-916-4	Sequence 4, Appli
18	1030.5	78.2	530	3 US-08-485-372A-4	Sequence 4, Appli
19	1030.5	78.2	530	4 US-09-409-006A-4	Sequence 4, Appli
20	1030.5	78.2	530	4 US-08-484-681-4	Sequence 4, Appli
21	1030.5	78.2	530	5 PCT-US93-07422-4	Sequence 4, Appli
22	1029	78.1	203	3 US-08-284-391B-31	Sequence 31, Appli
23	1029	78.1	203	3 US-09-218-950-31	Sequence 31, Appli
24	1029	78.1	398	2 US-08-284-391B-29	Sequence 29, Appli
25	1029	78.1	398	2 US-09-218-950-29	Sequence 29, Appli
26	1029	78.1	402	1 US-08-236-311-1	Sequence 1, Appli
27	1029	78.1	402	3 US-08-457-918-1	Sequence 1, Appli

28	1029	78.1	457	4 US-08-328-500-9	Sequence 9, Appli
29	1029	78.1	458	3 US-08-466-368-4	Sequence 4, Appli
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31	1029	78.1	462	2 US-08-284-391B-5	Sequence 5, Appli
32	1029	78.1	462	3 US-09-218-950-5	Sequence 5, Appli
33	1029	78.1	462	5 PCT-US92-01785-5	Sequence 5, Appli
34	1029	78.1	462	5 PCT-US95-00454-5	Sequence 5, Appli
35	1029	78.1	532	2 US-08-417-495-6	Sequence 6, Appli
36	1029	78.1	532	2 US-08-284-391B-6	Sequence 6, Appli
37	1029	78.1	532	3 US-09-218-950-6	Sequence 6, Appli
38	1029	78.1	532	5 PCT-US92-01785-6	Sequence 6, Appli
39	1029	78.1	532	5 PCT-US95-00454-6	Sequence 6, Appli
40	1029	78.1	532	2 US-08-417-495-4	Sequence 4, Appli
41	1029	78.1	532	2 US-08-284-391B-4	Sequence 4, Appli
42	1029	78.1	532	3 US-09-218-950-4	Sequence 4, Appli
43	1029	78.1	532	5 PCT-US92-01785-4	Sequence 4, Appli
44	1029	78.1	532	5 PCT-US95-00454-4	Sequence 4, Appli
45	1029	78.1	630	4 US-08-472-888A-6	Sequence 6, Appli
46	1023	77.7	295	6 5223394-9	Patent No. 5223394
47	1023	77.7	318	6 5223394-11	Patent No. 5223394
48	1023	77.7	458	3 US-09-039-555B-15	Sequence 15, Appli
49	1023	77.7	458	4 US-09-517-605-3	Sequence 3, Appli
50	1015	77.1	458	6 5223394-7	Patent No. 5223394
51	1012	76.8	394	3 US-08-466-368-2	Sequence 2, Appli
52	1012	76.8	394	3 US-08-328-500-2	Sequence 2, Appli
53	1003	76.2	394	6 5223418-2	Patent No. 5223418
54	916	69.6	434	1 US-08-236-311-4	Sequence 4, Appli
55	916	69.6	434	1 US-08-457-918-4	Sequence 4, Appli
56	914	69.4	410	3 US-08-630-172-17	Sequence 17, Appli
57	914	69.4	410	3 US-09-375-419-17	Sequence 17, Appli
58	899	68.3	433	3 US-09-100-409A-1	Sequence 1, Appli
59	899	68.3	903	1 US-08-021-601-12	Sequence 12, Appli
60	899	68.3	903	1 US-08-082-849B-12	Sequence 12, Appli
61	899	68.3	903	5 PCT-US94-01624-12	Sequence 12, Appli
62	898	68.2	433	2 US-08-867-149-1	Sequence 1, Appli
63	898	68.2	433	2 US-08-808-374-1	Sequence 1, Appli
64	718	54.5	433	6 5171838-13	Patent No. 5171838
65	716	54.4	138	3 US-08-630-172-1	Sequence 1, Appli
66	716	54.4	138	3 US-09-375-419-1	Sequence 1, Appli
67	595.5	45.2	376	2 US-08-558-269-10	Sequence 10, Appli
68	595.5	45.2	376	3 US-09-410-882-10	Sequence 10, Appli
69	589.5	44.8	383	2 US-08-558-269-6	Sequence 6, Appli
70	589.5	44.8	383	3 US-09-410-882-6	Sequence 6, Appli
71	494	37.5	94	3 US-08-466-368-5	Sequence 5, Appli
72	494	37.5	94	4 US-08-470-998-2	Sequence 2, Appli
73	494	37.5	94	4 US-08-328-500-10	Sequence 10, Appli
74	490.5	37.2	457	1 US-08-416-478A-8	Sequence 8, Appli
75	490.5	37.2	457	2 US-08-474-888B-8	Sequence 8, Appli
76	490.5	37.2	457	2 US-08-394-442B-8	Sequence 8, Appli
77	398	30.2	80	2 US-08-332-622A-84	Sequence 84, Appli
78	392	29.8	74	4 US-09-050-861B-8	Sequence 8, Appli
79	314	23.8	61	3 US-09-100-409A-20	Sequence 20, Appli
80	288	21.9	58	2 US-08-284-391B-35	Sequence 35, Appli
81	288	21.9	58	3 US-09-218-950-35	Sequence 35, Appli
82	228	17.3	46	3 US-09-100-409A-10	Sequence 10, Appli
83	228	17.3	81	3 US-09-100-409A-34	Sequence 34, Appli
84	212	16.1	154	3 US-08-630-172-7	Sequence 7, Appli
85	212	16.1	154	3 US-09-375-419-7	Sequence 7, Appli
86	211	16.0	40	3 US-09-100-409A-2	Sequence 2, Appli
87	211	16.0	42	3 US-09-100-409A-4	Sequence 4, Appli
88	211	16.0	77	3 US-09-100-409A-32	Sequence 32, Appli
89	200	15.2	41	6 5510256-5	Patent No. 5510256
90	168.5	12.8	81	2 US-08-332-622A-85	Sequence 85, Appli
91	167.5	12.7	81	2 US-08-332-622A-86	Sequence 86, Appli
92	167	12.7	34	3 US-09-100-409A-11	Sequence 11, Appli
93	167	12.7	39	3 US-09-100-409A-33	Sequence 33, Appli
94	156	11.8	29	3 US-09-100-409A-19	Sequence 19, Appli
95	151.5	11.5	47	3 US-09-303-323-92	Sequence 92, Appli
96	151.5	11.5	47	3 US-09-303-323-92	Sequence 92, Appli
97	151.5	11.5	47	4 US-09-770-014-92	Sequence 92, Appli
98	150	11.4	28	3 US-09-100-409A-3	Sequence 3, Appli
99	150	11.4	30	3 US-09-100-414B-91	Sequence 91, Appli
100	150	11.4	30	3 US-09-100-409A-5	Sequence 5, Appli

101 150 11.4 30 3 US-09-303-323-91 Sequence 91, Appl
102 150 11.4 30 4 US-09-770-014-91 Sequence 91, Appl
103 150 11.4 47 3 US-09-100-414B-93 Sequence 93, Appl
104 150 11.4 47 3 US-09-100-414B-94 Sequence 94, Appl
105 150 11.4 47 3 US-09-100-409A-60 Sequence 60, Appl
106 150 11.4 47 3 US-09-303-323-93 Sequence 93, Appl
107 150 11.4 47 3 US-09-303-323-94 Sequence 94, Appl
108 150 11.4 47 4 US-09-770-014-93 Sequence 93, Appl
109 150 11.4 47 4 US-09-770-014-94 Sequence 94, Appl
110 150 11.4 50 3 US-09-100-409A-37 Sequence 37, Appl
111 144 10.9 64 3 US-09-100-409A-35 Sequence 35, Appl
112 139 10.6 25 6 5171838-24 Patent No. 5171838
113 133 10.1 25 6 5171838-23 Patent No. 5171838
114 131 9.9 1260 4 US-08-506-296B-21 Sequence 21, Appl
115 129 9.8 308 2 US-08-414-657D-46 Sequence 46, Appl
116 129 9.8 325 2 US-08-414-657D-2 Sequence 2, Appl
117 129 9.8 325 2 US-08-414-657D-41 Sequence 41, Appl
118 129 9.8 325 4 US-09-135-080-2 Sequence 2, Appl
119 129 9.8 338 2 US-08-414-657D-60 Sequence 60, Appl
120 129 9.8 338 4 US-09-135-080-8 Sequence 8, Appl
121 129 9.8 338 4 US-09-976-594-404 Patent No. 5171838
122 127 9.6 24 6 5171838-22 Patent No. 5171838
123 126 9.6 315 2 US-08-414-657D-47 Sequence 47, Appl
124 126 9.6 338 2 US-08-414-657D-42 Sequence 42, Appl
125 126 9.6 338 2 US-08-414-657D-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1

US-08-477-460B-6

; Sequence 6, Application US/08477460B

; Patent No. 6034223

; GENERAL INFORMATION:

; APPLICANT: Progenics Pharmaceuticals, Inc.

; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,460B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/927,931

; FILING DATE: 07-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 977-9809

; TELEX: 422523 COOP UT

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 310 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-6

Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 NMRGVPRRLILVLQALIPATQGNKVILGKKGDPVELTCTASQKSTQFHMKNQIK 60
DB 1 NMRGVPRRLILVLQALIPATQGNKVILGKKGDPVELTCTASQKSTQFHMKNQIK 60
QY 61 IIGNGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNKIDSDTYICEVEDQKEEYOL 120
DB 61 IIGNGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNKIDSDTYICEVEDQKEEYOL 120
QY 121 LVFGLTANS DTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANS DTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCYVLQNKQKVEFEKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
DB 181 TWTCYVLQNKQKVEFEKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228
QY 241 SEFL 244
DB 229 VCLL 232

RESULT 2

US-08-379-516-6

; Sequence 6, Application US/08379516

; Patent No. 6083478

; GENERAL INFORMATION:

; APPLICANT: Allaway, Graham P.

; APPLICANT: Maddon, Paul J.

; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IGG2

; TITLE OF INVENTION: Immunconjugates and Uses Thereof

; FILE REFERENCE: 41215-A-PCT-US

; CURRENT APPLICATION NUMBER: US/08/379,516

; CURRENT FILING DATE: 1996-06-10

; EARLIER APPLICATION NUMBER: PCT/US93/07422

; EARLIER FILING DATE: 1993-08-06

; EARLIER APPLICATION NUMBER: 07/927,931

; EARLIER FILING DATE: 1992-08-07

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6

; LENGTH: 310

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-08-379-516-6

Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 NMRGVPRRLILVLQALIPATQGNKVILGKKGDPVELTCTASQKSTQFHMKNQIK 60
DB 1 NMRGVPRRLILVLQALIPATQGNKVILGKKGDPVELTCTASQKSTQFHMKNQIK 60
QY 61 IIGNGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNKIDSDTYICEVEDQKEEYOL 120
DB 61 IIGNGSFLTKGPSKLNDRADSRSLMDQGNFPLIIKNKIDSDTYICEVEDQKEEYOL 120
QY 121 LVFGLTANS DTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANS DTHLLOGQSITLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCYVLQNKQKVEFEKIDIVPRASALPAPPTGSALPDPTASALPDPPASALPALAVI 240
DB 181 TWTCYVLQNKQKVEFEKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228

QY 241 SFL 244
DB 229 VCLL 232

RESULT 3
US-09-329-916-6
; Sequence 6, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-09-329-916-6

Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVPFRHLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSSTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSSTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNGKVEFKIDIVRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 240

DB 181 TWTCTVLQNGKVEFKIDIVRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 228
QY 241 SFL 244
DB 229 VCLL 232

RESULT 4
US-08-485-372A-6
; Sequence 6, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-485-372A-6

Query Match 78.8%; Score 1038; DB 3; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVPFRHLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
DB 1 MNRGVPFRHLVLTQALLPAATQGNKVVLGKGGDTVELTCTASOKKSIOFHMKNNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVQL 120
QY 121 LVFGLTANSSTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSSTHLLQGGSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNGKVEFKIDIVRASALPAPPTGSALPDQGTASALPDPPAASALPALAVI 240

Db 181 TWCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228
QY 241 SFLL 244
Db 229 VCLL 232

RESULT 5

US-09-409-006A-6
Sequence 6, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-6

Query Match 78.8%; Score 1038; DB 4; Length 310;
Best Local Similarity 85.7%; Pred. No. 3,5e-80;

Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVFRRHLVLVQLALPAATQGNKVLGKKGDTVELTCTASOKKSIQPHMKNNOIK 60
Db 1 MNRGVFRRHLVLVQLALPAATQGNKVLGKKGDTVELTCTASOKKSIQPHMKNNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVOL 120
Db 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
Db 121 LVFGLTANSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWCTVLQNKQKVEFKIDIVPRASALPAPTGSALPDPTASALPDPPAASALPALAVI 240

Db 181 TWCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228
QY 241 SFLL 244
Db 229 VCLL 232

RESULT 6

US-08-484-681-6
Sequence 6, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-6

Query Match 78.8%; Score 1038; DB 4; Length 310;
Best Local Similarity 85.7%; Pred. No. 3,5e-80;

Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

QY 1 MNRGVFRRHLVLVQLALPAATQGNKVLGKKGDTVELTCTASOKKSIQPHMKNNOIK 60
Db 1 MNRGVFRRHLVLVQLALPAATQGNKVLGKKGDTVELTCTASOKKSIQPHMKNNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVOL 120
Db 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
Db 121 LVFGLTANSDTHLLQGSILTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWCTVLQNKQKVEFKIDIVPRASALPAPTGSALPDPTASALPDPPAASALPALAVI 240
Db 181 TWCTVLQNKQKVEFKIDIVLAFVTAAP-----SVFIFFPSDEQLKSGTASV 228

Qy 241 SFLL 244
Db 229 VCUL 232

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RESULT 7
PCT-US93-07422-6
; Sequence 6, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07422
; FILING DATE: 19930806
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; PCT-US93-07422-6
```

Query Match 78.8%; Score 1038; DB 5; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e-80;
Matches 209; Conservative 4; Mismatches 19; Indels 12; Gaps 1;

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Qy 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
Db 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
Qy 61 ILNQGSEFLTKGSKLNDRAISRSLMDQGNFPLIINKLTIKESDPTICVEBOQKEVOL 120
Db 61 ILNQGSEFLTKGSKLNDRAISRSLMDQGNFPLIINKLTIKESDPTICVEBOQKEVOL 120
Qy 121 LVEGLTANSPTHLTQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLISVSOLELQDSG 180
Db 121 LVEGLTANSPTHLTQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLISVSOLELQDSG 180
Qy 181 TWICTVLQONQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
Db 181 TWICTVLQONQKVEFKIDIVLAFTVAAP-----SVFIFFPSDEQLKSGTASV 228
Qy 241 SFLL 244
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Db 229 VCUL 232

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RESULT 8
US-08-477-4608-2
; Sequence 2, Application US/084774608
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,4608
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-08-477-4608-2
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Query Match 78.4%; Score 1032.5; DB 3; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.1e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

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Qy 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
Db 1 MNRGVPFRHLLVLVQLALLPAATQGNKRVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
Qy 61 ILNQGSEFLTKGSKLNDRAISRSLMDQGNFPLIINKLTIKESDPTICVEBOQKEVOL 120
Db 61 ILNQGSEFLTKGSKLNDRAISRSLMDQGNFPLIINKLTIKESDPTICVEBOQKEVOL 120
Qy 121 LVEGLTANSPTHLTQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLISVSOLELQDSG 180
Db 121 LVEGLTANSPTHLTQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLISVSOLELQDSG 180
Qy 181 TWICTVLQONQKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPA 230
Db 181 TWICTVLQONQKVEFKIDIVLAFFERKCCVECP-----CPAPVA 221
```

RESULT 9
US-08-379-516-2
Sequence 2, Application US/08379516
Patent No. 6083478
GENERAL INFORMATION:
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
EARLIER FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER FILING DATE: 1993-08-06
EARLIER APPLICATION NUMBER: 07/927,931
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
US-08-379-516-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVLTCTASOKKSIQFMKNSNQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVLTCTASOKKSIQFMKNSNQIK 60
QY 61 ILGNQSSFLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEQKEVQL 120
DB 61 ILGNQSSFLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEQKEVQL 120
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKVKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWTCTVLQNKVKVEFKIDIVLAFERKCCVCECP-----CPAPVA 221

RESULT 10
US-09-329-916-2
Sequence 2, Application US/09329916
Patent No. 6177549
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,460
FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-329-916-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVLTCTASOKKSIQFMKNSNQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDVLTCTASOKKSIQFMKNSNQIK 60
QY 61 ILGNQSSFLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEQKEVQL 120
DB 61 ILGNQSSFLTKGSPKINDRADSRSLMDQGNFPLIINKIKIEDSDTYICEVEQKEVQL 120
QY 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKVKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWTCTVLQNKVKVEFKIDIVLAFERKCCVCECP-----CPAPVA 221

RESULT 11
US-08-485-372A-2
Sequence 2, Application US/08485372A
Patent No. 6187748
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-485-372A-2

Query Match 78.4%; Score 1032.5; DB 3; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
DB 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
QY 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVSOLELDSG 180
DB 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVSOLELDSG 180
QY 181 TWICTVLQNKQKVEFKIDIV----PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWICTVLQNKQKVEFKIDIVLAFERKCCVCECP-----CPAPPA 221

RESULT 12
US-09-409-006A-2
Sequence 2, Application US/09409006A
Patent No. 6342586
GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-09-409-006A-2

Query Match 78.4%; Score 1032.5; DB 4; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
DB 1 MNRGVPFRHLVLVQLALLPAATQGNKVLGKGGDTVELTCTASOKKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
DB 61 ILGNQGSFLTKGPKSKINDRADSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
QY 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVSOLELDSG 180
DB 121 LVFGLTANSDPHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLSSVSOLELDSG 180
QY 181 TWICTVLQNKQKVEFKIDIV----PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWICTVLQNKQKVEFKIDIVLAFERKCCVCECP-----CPAPPA 221

RESULT 13
US-08-484-681-2
Sequence 2, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
TITLE OF INVENTION: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-2

Query Match 78.4%; Score 1032.5; DB 4; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRHLVLQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVFRRHLVLQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLQGSGLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELODSG 180
DB 121 LVFGLTANSDTHLQGSGLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELODSG 180
QY 181 TWICTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWICTVLQNKQKVEFKIDIVLAFERKCCVECP-----CPAPVA 221

RESULT 14

PCT-US93-07422-2

Sequence 2, Application PC/TUS9307422

GENERAL INFORMATION:

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07422

FILING DATE: 19930806

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

ORGANISM: homo sapien

CELL TYPE: lymphocyte

PCT-US93-07422-2

Query Match 78.4%; Score 1032.5; DB 5; Length 432;
Best Local Similarity 88.0%; Pred. No. 1.6e-79;
Matches 206; Conservative 1; Mismatches 10; Indels 17; Gaps 2;

QY 1 MNRGVFRRHLVLQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
DB 1 MNRGVFRRHLVLQALLPATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNSNQIK 60
QY 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSKLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLQGSGLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELODSG 180
DB 121 LVFGLTANSDTHLQGSGLTLTLESPPGSSPSVQCSPRGKNIQGGKTLVSQLELODSG 180
QY 181 TWICTVLQNKQKVEFKIDIV---PRASALPAPPTGSALPDPTASALPDPPAA 230
DB 181 TWICTVLQNKQKVEFKIDIVLAFERKCCVECP-----CPAPVA 221

RESULT 15

US-08-477-460B-4

Sequence 4, Application US/08477460B

Patent No. 6034223

GENERAL INFORMATION:

APPLICANT: Progenics Pharmaceuticals, Inc.

TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED

TITLE OF INVENTION: CD4-GAMMA2 AND CD4-19G2 IMMUNOCONJUGATES, AND USES THEREOF

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,460B

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPM/AJM

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 977-9809

TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

ORGANISM: homo sapien

CELL TYPE: lymphocyte

Query Match 78.2%; Score 1030.5; DB 3; Length 530;
Best Local Similarity 84.8%; Pred. No. 3.1e-79;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

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QY 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
DB 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
DB 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
QY 241 SFL 244
DB 241 SFL 244
QY 230 GCLV 233
DB 230 GCLV 233
```

RESULT 16

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US-08-379-516-4
; Sequence 4, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Madden, Paul J.
; TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
; TITLE OF INVENTION: Immunocjugates and Uses Thereof
; FILE REFERENCE: 41215-A-PCT-US
; CURRENT APPLICATION NUMBER: US/08/379,516
; EARLIER FILING DATE: 1996-06-10
; EARLIER APPLICATION NUMBER: PCT/US93/07422
; EARLIER FILING DATE: 1993-08-06
; EARLIER APPLICATION NUMBER: 07/927,931
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-379-516-4
```

Query Match 78.2%; Score 1030.5; DB 3; Length 530;

Best Local Similarity 84.8%; Pred. No. 3.1e-79;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

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QY 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
DB 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
DB 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
QY 241 SFL 244
DB 241 SFL 244
QY 230 GCLV 233
DB 230 GCLV 233
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RESULT 17

US-09-329-916-4

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; Sequence 4, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/329,916
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,460
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo. sapien
; CELL TYPE: lymphocyte
US-09-329-916-4
```

Query Match 78.2%; Score 1030.5; DB 3; Length 530;

Best Local Similarity 84.8%; Pred. No. 3.1e-79;

Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

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QY 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
DB 1 MNRGVPFRHLILVQLALLPAATGKNVVLGKKDVTVELTCTASQKKSIOFHMNSNQIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSPTHLLOGOSLTLTLESPPGSSPVQCRSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
DB 181 TWICTVQONQKVEFKIDIVPRASALPAPPTGSALPDPQTASALPDPAPASALPALAVI 240
QY 241 SFL 244
DB 241 SFL 244
QY 230 GCLV 233
DB 230 GCLV 233
```

RESULT 18
US-08-485-372A-4
; Sequence 4, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-08-485-372A-4

Query Match 78.2%; Score 1030.5; DB 3; Length 530;
Best Local Similarity 84.8%; Pred. No. 3.1e-79;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;
QY 1 MNRGVPRHLLVQLALPAAATGKGVVGLGKKGDTVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPAAATGKGVVGLGKKGDTVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGSPSKINDRADSRSLMDQGNFPLIKNLKIEBDDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKINDRADSRSLMDQGNFPLIKNLKIEBDDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNTIOGKTLSSVQLELQDSG 180
DB 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNTIOGKTLSSVQLELQDSG 180
QY 181 TWICTVLQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWICTVLQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233

RESULT 19
US-09-409-006A-4
; Sequence 4, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
; APPLICANT: Progenice Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,006A
; FILING DATE: 29-SEP-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
; US-09-409-006A-4

Query Match 78.2%; Score 1030.5; DB 4; Length 530;
Best Local Similarity 84.8%; Pred. No. 3.1e-79;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;
QY 1 MNRGVPRHLLVQLALPAAATGKGVVGLGKKGDTVELTCTASQKKSIOFHMKNNSQIK 60
DB 1 MNRGVPRHLLVQLALPAAATGKGVVGLGKKGDTVELTCTASQKKSIOFHMKNNSQIK 60
QY 61 ILGNQGSFLTKGSPSKINDRADSRSLMDQGNFPLIKNLKIEBDDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPSKINDRADSRSLMDQGNFPLIKNLKIEBDDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNTIOGKTLSSVQLELQDSG 180
DB 121 LVFGLTANSDTHLLOQOSLTLTLESPPGSSPSVQCRSPRGKNTIOGKTLSSVQLELQDSG 180
QY 181 TWICTVLQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWICTVLQOKKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233

RESULT 20

US-08-484-681-4
Sequence 4, Application US/08484681
Patent No. 6451313
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
US-08-484-681-4

Query Match 78.2%; Score 1030.5; DB 4; Length 530;
Best Local Similarity 84.8%; Pred. No. 3.1e-79;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
QY 61 ILNGQSFLLTKGPKSKLNDRAISRSLMDQGNFPLIINKLIEBDDTYICEVEDQKEVOL 120
DB 61 ILNGQSFLLTKGPKSKLNDRAISRSLMDQGNFPLIINKLIEBDDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCITVLOQOKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWTCITVLOQOKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233

RESULT 21
PCT-US93-07422-4

Sequence 4, Application PC/TUS9307422

GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 19930806
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422323 COOP UT
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: lymphocyte
PCT-US93-07422-4

Query Match 78.2%; Score 1030.5; DB 5; Length 530;
Best Local Similarity 84.8%; Pred. No. 3.1e-79;
Matches 207; Conservative 5; Mismatches 21; Indels 11; Gaps 1;

QY 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVPRRLHLLVQLALPAAATQGNKVVLGKGGDTVELTCTASQKKSIOFHMKNNOIK 60
QY 61 ILNGQSFLLTKGPKSKLNDRAISRSLMDQGNFPLIINKLIEBDDTYICEVEDQKEVOL 120
DB 61 ILNGQSFLLTKGPKSKLNDRAISRSLMDQGNFPLIINKLIEBDDTYICEVEDQKEVOL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCITVLOQOKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
DB 181 TWTCITVLOQOKVEFKIDIVPRASALPAPPTGSALPDPTASALPDPPAASALPALAVI 240
QY 241 SFL 244
DB 230 GCLV 233

RESULT 22
US-08-284-391B-31
Sequence 31, Application US/08284391B

```
Patent No. 5851828
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-391B-31

Query Match      78.1%; Score 1029; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1,1e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDTVELTCTASOKKSIQFHMKNNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDTVELTCTASOKKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 23
US-09-218-950-31
Sequence 31, Application US/09218950
```

```
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-950-31

Query Match      78.1%; Score 1029; DB 3; Length 203;
Best Local Similarity 100.0%; Pred. No. 1,1e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDTVELTCTASOKKSIQFHMKNNSQIK 60
DB 1 MNRGVPRHLLVLTQALLPAATQGNKVVLGKKGDTVELTCTASOKKSIQFHMKNNSQIK 60
QY 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLLTKGSKLNDRAADSRSLMDQGNFPLIINKLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDTHLLQGSQSLTLTLESPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200

RESULT 24
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US-08-284-391B-29
Sequence 29, Application US/08284391B
Patent No. 5851828
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-391B-29

Query Match 78.1%; Score 1029; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVQLALLPAATGKNRVLGKGGDTVELTCTASOKKSIOFHMNSNOIK 60
DB 1 MNRGVPFRHLLVQLALLPAATGKNRVLGKGGDTVELTCTASOKKSIOFHMNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200

RESULT 25

US-09-218-950-29
Sequence 29, Application US/09218950
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
FILING DATE: 02-AUG-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-218-950-29

Query Match 78.1%; Score 1029; DB 3; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLLVQLALLPAATGKNRVLGKGGDTVELTCTASOKKSIOFHMNSNOIK 60
DB 1 MNRGVPFRHLLVQLALLPAATGKNRVLGKGGDTVELTCTASOKKSIOFHMNSNOIK 60
QY 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGPKSLNDRADSRSLMDQGNFPLIINKLIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLLOQGSLLTLESPPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNOQKVEFKIDIV 200
DB 181 TWTCTVLQNOQKVEFKIDIV 200

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RESULT 26
US-08-236-311-1
; Sequence 1, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Haasek, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-1

Query Match      78.1%; Score 1029; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALPPATQGNKVVIGKKGDVVELTCTASQKKSIOFHMNSNQIK 60
DB 1 MNRGVPFRHLILVQLALPPATQGNKVVIGKKGDVVELTCTASQKKSIOFHMNSNQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADRSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADRSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLIQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLIQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
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RESULT 27
US-08-457-918-1
; Sequence 1, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-1

Query Match      78.1%; Score 1029; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 2.8e-79;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLILVQLALPPATQGNKVVIGKKGDVVELTCTASQKKSIOFHMNSNQIK 60
DB 1 MNRGVPFRHLILVQLALPPATQGNKVVIGKKGDVVELTCTASQKKSIOFHMNSNQIK 60
QY 61 ILGNQGSFLTKGSPKLNDRADRSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
DB 61 ILGNQGSFLTKGSPKLNDRADRSRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVOL 120
QY 121 LVFGLTANSPTHLIQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
DB 121 LVFGLTANSPTHLIQGOSLTLTLSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDQSG 180
QY 181 TWTCTVLQNKQKVEFKIDIV 200
DB 181 TWTCTVLQNKQKVEFKIDIV 200
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